

=> d his

(FILE 'HOME' ENTERED AT 12:08:36 ON 05 APR 2004)

FILE 'DISSABS, IMOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 12:08:46 ON
05 APR 2004

E 'SAINT-REMY' 'JEAN-MARIE'?/AU

E SAINT-REMY JEAN-MARIE?/AU

E JACQUEMIN MARC?/AU

L1 50 S E1 OR E2
L2 652376 S (SYSTEMIC INFLAMMATORY RESPONSE SYNDROME) OR SIRS OR SEPSIS O
L3 100225 S FACTOR (A) VIII
L4 3552 S (ANTI OR ANTIBOD?) (A) L3
L5 29 S L4 (S) L2
L6 20 DUP REM L5 (9 DUPLICATES REMOVED)

=>

WEST Search History

Hide Items

Restore

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DATE: Monday, April 05, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
<input type="checkbox"/>	L13	L11 same l4	5
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<input type="checkbox"/>	L9	L5 same l4	159
<input type="checkbox"/>	L8	L5 same l3	8
<input type="checkbox"/>	L7	L6 same l3	1
<input type="checkbox"/>	L6	(anti or antibod\$) adj L5	275
<input type="checkbox"/>	L5	factor adj (VIII or V)	8473
<input type="checkbox"/>	L4	sepsis or septic or thrombus	36439
<input type="checkbox"/>	L3	(systemic inflammatory response syendrome) or SIRS	40826
<input type="checkbox"/>	L2	Jacquemin-marc-\$.in.	4
<input type="checkbox"/>	L1	'Saint-remy'-'Jean-Marie'-\$in.	4

END OF SEARCH HISTORY

L6 ANSWER 8 OF 20 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 1999:465724 CAPLUS

DOCUMENT NUMBER: 131:115050

TITLE: Antibodies against factor VIII in patients with solid tumors. Successful treatment of cancer may suppress inhibitor formation

AUTHOR(S): Sallah, Sabah; Singh, Paramjeet; Hanrahan, L. Robert

CORPORATE SOURCE: Department Medicine, Division Hematology/Oncology, Univ. Tennessee, Memphis, TN, 38163, USA

SOURCE: Haemostasis (1998), 28(5), 244-249

CODEN: HMTSB7; ISSN: 0301-0147

PUBLISHER: S. Karger AG

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In 1995-1998, the authors treated 5 patients with anti-factor VIII antibodies and spontaneous bleeding. All patients had underlying malignant conditions. Initial control of the bleeding episodes and reduction in inhibitor titer was achieved in all patients. Disappearance of factor VIII inhibitor occurred in 3 patients after either resection of the tumor or chemotherapy. Immunosuppression therapy failed to eradicate the antibody in 2 patients with metastatic disease. Antibodies against factor VIII appearing in certain patients may be directly associated with the underlying malignancy, rather than a coincidental finding. Attempts to reduce the titer or eradicate the inhibitor may fail if recognition of the underlying condition is not sought, or an appropriate treatment of cancer is not offered. Antibodies against factor VIII developing in previously healthy individuals constitute the most common spontaneous inhibitors of any clotting factor. Accurate ests. of the incidence of **anti-factor VIII** inhibitors are not available, since some of these antibodies may not be associated with bleeding, or the condition may be misinterpreted as **disseminated intravascular coagulation**, especially when it is associated with known underlying malignancy. About 50% of anti-factor VIII antibodies developing in the nonhemophilic population occur in otherwise healthy individuals over the age of 50 yr. Other conditions associated with the development of these inhibitors, in decreasing frequency, include autoimmune diseases, peripartum period, lymphoproliferative disorders, solid tumors and reaction to certain medications [1]. Patients with antibodies against factor VIII usually present with spontaneous bleedings involving soft tissues, retropharyngeal or retroperitoneal spaces, intracerebral or other types of serious hemorrhagic episodes. The most common laboratory abnormality is prolongation of PTT and decreased to absent factor VIII activity. Among the most commonly used products to manage patients with bleeding episodes and autoantibodies against factor VIII are high-dose human factor VIII, and inhibitor by-passing agents. Decreasing the inhibitor titer may also be achieved via plasma exchange and immuno-suppression. The formation of factor VIII antibodies in patients with solid tumors in terms of its course, response to treatment, and prognosis has not been addressed. We describe in this article the occurrence and the course of anti-factor VIII antibodies in 5 patients with solid malignancies.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN T

ACCESSION NUMBER: 2001:70012 CAPLUS
DOCUMENT NUMBER: 135:32107
TITLE: Transient factor VIII inhibitor in a hemophilia
patient after staphylococcal septic shock syndrome
AUTHOR(S): Yamamoto, Kazuhiko; Niiya, Kenji; Shigematu, Terunobu;
Kiguchi, Toru; Takenaka, Katsuto; Shinagawa, Katsushi;
Ishimaru, Fumihiko; Ikeda, Kazuma; Shima, Midori;
Harada, Mine
CORPORATE SOURCE: Second Department of Medicine, Okayama University
Medical School, Okayama, 700-8558, Japan
SOURCE: International Journal of Hematology (2000), 72(4),
517-519
CODEN: IJHEEY; ISSN: 0925-5710
PUBLISHER: Carden Jennings Publishing
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We report a transient type I factor VIII inhibitor that arose in a 30-yr-old hemophilia patient just after staphylococcal septicemia. This situation usually occurs early in the course of substitution therapy with factor VIII concentrate in hemophilia patients. Although disseminated intravascular coagulation and acute respiratory distress syndrome developed after septic shock, the patient recovered following i.v. administration of antibiotics (meropenem and gentamycin), an antithrombin preparation, high-dose methylprednisolone, and recombinant factor VIII concentrate (rFVIII). During this therapy, however, activated partial thromboplastin time gradually lengthened. On the seventh day of hospitalization, intracranial hemorrhage occurred with right hemiplegia, even though the substitution therapy had continued at the same dosage (30 U/kg per day) of rFVIII. At that point, 4 Bethesda units of the type I inhibitor against factor VIII were detected in the plasma. Increased amts. (46 U/kg per day) of rFVIII and prednisolone were administered, and hypothermic therapy was initiated. Following these treatments, the patient's general condition gradually improved, and within 25 days the inhibitor titer dropped to undetectable levels and did not recur during treatment. These clin. findings suggest that the staphylococcal septic shock may have acted as a trigger in the development of transient factor VIII inhibitor in this patient.

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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:36:42 ; Search time 12.824 Seconds
(without alignments)

575.678 Million cell updates/sec

Title: US-10-044-569B-8

Perfect score: 738

Sequence: 1 METPAQLLFLLLMLPDTTG.....TKVEIKRTVAAPSVFIFFPS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666.5	90.3	235	4	US-09-472-087-14
2	666.5	90.3	235	4	US-09-472-087-65
3	654.5	88.7	233	4	US-09-472-087-15
4	654.5	88.7	233	4	US-09-472-087-67
5	649.5	88.0	150	3	US-08-862-124-5
6	645	87.4	234	4	US-09-472-087-17
7	645	87.4	234	4	US-09-472-087-69
8	604	81.8	134	1	US-08-405-034-4
9	593.5	79.1	129	2	US-08-480-774A-4
10	575	77.9	226	4	US-09-456-090A-42
11	571	77.4	226	4	US-09-456-090A-86
12	571	77.4	226	4	US-09-456-090A-86
13	569	77.1	226	4	US-09-456-090A-86
14	567	76.8	224	4	US-09-456-090A-52
15	566	76.7	226	4	US-09-456-090A-72
16	564	76.4	116	1	US-08-031-131-183
17	564	76.4	116	2	US-08-036-762-183
18	564	76.4	116	3	US-08-036-762-183
19	564	76.4	116	4	US-08-758-417A-311
20	564	76.4	116	4	US-09-456-090A-38
21	560	75.9	234	3	US-09-049-672A-6
22	559	75.7	226	4	US-09-456-090A-74
23	554	75.1	224	4	US-09-456-090A-76
24	553	74.9	224	4	US-09-456-090A-44
25	553	74.9	224	4	US-09-456-090A-78
26	549	74.4	224	4	US-09-456-090A-40
27	545	73.8	235	3	US-08-812-586-16

28 545 73.8 235 4 US-09-535-832A-17 Sequence 17, Appl
29 539.5 73.1 141 4 US-09-472-087-88 Sequence 88, Appl
30 531.5 72.0 304 3 US-08-862-124-14 Sequence 14, Appl
31 529 71.7 146 4 US-09-472-087-21 Sequence 21, Appl
32 529 71.7 146 4 US-09-472-087-93 Sequence 93, Appl
33 527.5 71.5 141 4 US-09-472-087-89 Sequence 89, Appl
34 524.5 71.1 235 1 US-08-276-852-153 Sequence 153, Appl
35 524.5 71.1 235 1 US-08-899-575-153 Sequence 153, Appl
36 524.5 71.1 235 5 PCT-US95-08743-153 Sequence 153, Appl
37 523 70.9 215 2 US-08-480-753-8 Sequence 8, Appl
38 523 70.5 239 3 US-08-812-586-29 Sequence 29, Appl
39 520.5 70.5 239 4 US-09-535-832A-30 Sequence 30, Appl
40 519 70.3 139 4 US-09-472-087-16 Sequence 16, Appl
41 519 70.3 139 4 US-09-472-087-90 Sequence 90, Appl
42 518 70.2 142 4 US-09-472-087-91 Sequence 91, Appl
43 517 70.1 224 4 US-09-456-090A-84 Sequence 84, Appl
44 516.5 70.0 287 3 US-08-862-124-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match 90.3%; Score 666.5; DB 4; Length 235;
Best Local Similarity 91.6%; Ered. No. 1.3e-55;
Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
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DB 1 METPAQLLFLLLMLPDTTGTVILTPFPGLTSLSPGERATLSCRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGAASSRATDIPHRFGSGSGTDTITISRLPEDFAVYCCQYGTSAITTF 120
DB 61 PQAPRLIYGAASSRATDIPHRFGSGSGTDTITISRLPEDFAVYCCQYGTSAITTF 119
QY 121 GGGTKVEIKRTVAAPSVFIFFPS 143
DB 120 GGGTKVEIKRTVAAPSVFIFFPS 142

RESULT 2
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.

```

; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      90.3%; Score 666.5; DB 4; Length 235;
Best Local Similarity 91.6%; Pred. No. 1.8e-55;
Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

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Db      1  METPAQLLFLLLLWLPDITGIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60

Qy      61  PQAPRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCOYGTSALLTF 120
Db      61  PQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCOYGTSALLTF 119

Qy      121  GGGTKVEIKRTVAAPSVFIIPPS 143
Db      120  GGGTKVEIKRTVAAPSVFIIPPS 142

RESULT 3
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15

Query Match      89.7%; Score 654.5; DB 4; Length 233;
Best Local Similarity 91.6%; Pred. No. 1.8e-54;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

Qy      1  METPAQLLFLLLLWLPDITGIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60
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Qy      61  PQAPRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCOYGTSALLTF 120
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Qy      59  PQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCOYGISP-FTF 117
Db      59  PQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCOYGISP-FTF 117

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Qy      121  GGGTKVEIKRTVAAPSVFIIPPS 143
Db      118  GGGTKVEIKRTVAAPSVFIIPPS 140

RESULT 4
US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-67

Query Match      88.7%; Score 654.5; DB 4; Length 233;
Best Local Similarity 91.6%; Pred. No. 1.8e-54;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

Qy      1  METPAQLLFLLLLWLPDITGIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60
Db      1  METPAQLLFLLLLWLPDITGIVLTQPGTSLSPGERATLSCRT--SVSSSYLAWYQOK 58

Qy      61  PQAPRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCOYGTSALLTF 120
Db      59  PQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCOYGISP-FTF 117

Qy      121  GGGTKVEIKRTVAAPSVFIIPPS 143
Db      118  GGGTKVEIKRTVAAPSVFIIPPS 140

RESULT 5
US-08-862-124-5
; Sequence 5, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-862-124-5
Query Match 88.0%; Score 649.5; DB 3; Length 150;
Best Local Similarity 87.7%; Pred. No. 3.2e-54;
Matches 128; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

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Qy 118 LTGGGKVEIKRTVAAPSVFIIPPS 143
Db 125 ITFGGKVEIKRTVAAPSVFIIPPS 150

RESULT 6
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-17
Query Match 87.4%; Score 645; DB 4; Length 234;
Best Local Similarity 90.9%; Pred. No. 1.4e-53;
Matches 130; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

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Db 1 METPAQLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSV--SSYLAWYQOK 59
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Db 60 PGQAPRLLIYGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGISP-FTF 118
Qy 121 GGGTKVEIKRTVAAPSVFIIPPS 143
Db 119 GPGTKVDIKRTVAAPSVFIIPPS 141

RESULT 7
US-09-472-087-69
; Sequence 69, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-69
Query Match 87.4%; Score 645; DB 4; Length 234;
Best Local Similarity 90.9%; Pred. No. 1.4e-53;
Matches 130; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

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Db 1 METPAQLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSV--SSYLAWYQOK 59
Qy 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGTSSALLTF 120
Db 60 PGQAPRLLIYGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGISP-FTF 118
Qy 121 GGGTKVEIKRTVAAPSVFIIPPS 143
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RESULT 8
US-08-405-034-4
; Sequence 4, Application US/08405034
; Patent No. 5744585
; Patent No. 5744585 5712371
; GENERAL INFORMATION:
; APPLICANT: Medenica, Rajko D.
; APPLICANT: Mukerjee, Sonjoy
; TITLE OF INVENTION: Human Monoclonal Antibody Against Lung
; TITLE OF INVENTION: Carcinoma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25	REGISTRATION NUMBER: 34,235
CURRENT APPLICATION DATA:	REFERENCE/DOCKET NUMBER: 41450-FWC-DIV
APPLICATION NUMBER: US/08/405,034	TELECOMMUNICATION INFORMATION:
FILING DATE:	TELEPHONE: 617-523-3400
CLASSIFICATION: 530	TELEFAX: 617-523-6440
ATTORNEY/AGENT INFORMATION:	TELEX:
NAME: Sara, Charles S.	INFORMATION FOR SEQ ID NO: 4:
REGISTRATION NUMBER: 30,492	SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: 34656.009	LENGTH: 129 amino acids
TELECOMMUNICATION INFORMATION:	TYPE: amino acid
TELEPHONE: 608-831-2100	STRANDEDNESS: single
TELEFAX: 608-831-2106	TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: 4:	MOLECULE TYPE: protein
SEQUENCE CHARACTERISTICS:	FRAGMENT TYPE: internal
LENGTH: 134 amino acids	US-08-405-034-4
TYPE: amino acid	
TOPOLOGY: linear	Query Match 81.8%; Score 604; DB 1; Length 134;
MOLECULE TYPE: protein	Best Local Similarity 88.1%; Pred. No. 5.5e-50;
US-08-405-034-4	Matches 118; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Query Match 81.8%; Score 604; DB 1; Length 134;	Query Match 79.1%; Score 583.5; DB 2; Length 129;
Best Local Similarity 88.1%; Pred. No. 5.5e-50;	Best Local Similarity 89.2%; Pred. No. 4.6e-48;
Matches 118; Conservative 6; Mismatches 10; Indels 0; Gaps 0;	Matches 116; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
QY 1 METPAQLFLLLMLPDTTGEIVLTQFCTLSLSPGERATISCRASQSVASAYLAWYQOK 60	QY 1 METPAQLFLLLMLPDTTGEIVLTQFCTLSLSPGERATISCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLMLPDTTGEIVLTQFCTLSLSPGERATISCRASQSVASAYLAWYQOK 60	DB 1 METPAQLFLLLMLPDTTGEIVLTQFCTLSLSPGERATISCRASQSVASAYLAWYQOK 60
QY 61 PQOAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120	QY 61 PQOAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 61 PQOAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120	DB 61 PQOAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
QY 121 GGGTKVEIKRTVAA 134	QY 121 GGGTKVEIKR 130
DB 121 GGGTKLEIKRTVAA 134	DB 120 GGGTKLEIKR 129
RESULT 9	RESULT 10
US-08-480-774A-4	US-09-456-090A-42
Sequence 4, Application US/08480774A	Sequence 42, Application US/09456090A
Patent No. 5852186	Patent No. 6680209
GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: MARASCO, Wayne A.	APPLICANT: Buechler, Joe
APPLICANT: SODROSKI, Joseph G.	APPLICANT: Valkirs, Gunars
APPLICANT: HASELTINE, William A.	APPLICANT: Gray, Jeff
APPLICANT: POSNER, Marshall R.	APPLICANT: Lomborg, Nils
TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN	TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
TITLE OF INVENTION: ANTI-GP 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME	FILE REFERENCE: 020015-000200US
TITLE OF INVENTION: AND USE THEREOF	CURRENT APPLICATION NUMBER: US/09/456,090A
NUMBER OF SEQUENCES: 16	CURRENT FILING DATE: 1999-12-06
CORRESPONDENCE ADDRESS:	NUMBER OF SEQ ID NOS: 110
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP	SOFTWARE: PatentIn Ver. 2.1
STREET: 130 Water Street	SEQ ID NO 42
CITY: Boston	LENGTH: 226
STATE: MA	TYPE: PRT
COUNTRY: USA	ORGANISM: Homo sapiens
ZIP: 02109	OTHER INFORMATION: M1-5L
COMPUTER READABLE FORM:	US-09-456-090A-42
MEDIUM TYPE: Diskette	
COMPUTER: IBM Compatible	Query Match 77.9%; Score 575; DB 4; Length 226;
OPERATING SYSTEM: DOS	Best Local Similarity 90.2%; Pred. No. 5.7e-47;
SOFTWARE: FastSeq for Windows Version 2.0	Matches 111; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/480,774A	QY 21 EIVLTQFCTLSLSPGERATISCRASQSVASAYLAWYQOKPQOAPRLIYGASSRATDIP 80
FILING DATE: 07-JUN-1995	DB 1 EIVMTQSPGTLSLSPGERATISCRASQSVSSSYLAWYQOKPQOAPRLIYGASSRATGIP 60
CLASSIFICATION: 435	QY 81 HRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGKTVEIKRTVAAPSVPFIF 140
PRIOR APPLICATION DATA:	DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGKTVEIKRTVAAPSVPFIF 120
APPLICATION NUMBER: 08/400,674	QY 141 PPS 143
FILING DATE: 08-MAR-1995	DB 121 PPS 123
APPLICATION NUMBER: 07/804,652	
FILING DATE: 10-DEC-1991	
ATTORNEY/AGENT INFORMATION:	
NAME: Resnick, David S.	

```
US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match          77.4%; Score 571; DB 4; Length 226;
Best Local Similarity 91.1%; Pred. No. 1.4e-46;
Matches 112; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60

Qy 81 HRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 140
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 120

Qy 141 PPS 143
Db 121 PPS 123

RESULT 12
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match          77.4%; Score 571; DB 4; Length 226;
Best Local Similarity 91.1%; Pred. No. 1.4e-46;
Matches 112; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60

Qy 81 HRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 140
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 120

Qy 141 PPS 143
Db 121 PPS 123

US-09-456-090A-80
; Sequence 80, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-20L
US-09-456-090A-80

Query Match          77.1%; Score 569; DB 4; Length 226;
Best Local Similarity 89.4%; Pred. No. 2.1e-46;
Matches 110; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60

Qy 81 HRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 140
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTFGGGTKVEIKRTVAAPSVFIF 120

Qy 141 PPS 143
Db 121 PPS 123

RESULT 14
US-09-456-090A-52
; Sequence 52, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-25L
US-09-456-090A-52

Query Match          76.8%; Score 567; DB 4; Length 224;
Best Local Similarity 91.1%; Pred. No. 3.2e-46;
Matches 112; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 60
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QY 81 HRFSGSGGDTFTLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKRTVAAPSVFIF 140
 Db 61 NRFSGSGGDTFTLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKRTVAAPSVFIF 118
 QY 141 PPS 143
 Db 119 PPS 121

RESULT 15

US-09-456-090A-72
 ; Sequence 72 Application US/09456090A
 ; Patent No. 6680209
 ; GENERAL INFORMATION:
 ; APPLICANT: Buechler, Joe
 ; APPLICANT: Valkirs, Gunars
 ; APPLICANT: Gray, Jeff
 ; APPLICANT: Lonberg, Nils
 ; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
 ; FILE REFERENCE: 020015-000200US
 ; CURRENT APPLICATION NUMBER: US/09/456,090A
 ; CURRENT FILING DATE: 1999-12-06
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 72
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: M2-11L
 US-09-456-090A-72

Query Match 76.7%; Score 566; DB 4; Length 226;
 Best Local Similarity 89.4%; Pred. No. 4e-46;
 Matches 110; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 21 EIVLTQPPGTLISLSPGERATLSCRASQSVASAYLAWYQKPGQAPPELLIYGASSRATDIP 80
 Db 1 EIVNTQSPGTLISLSPGERATLSCRASQSVSSYLAAYQKPGQAPPELLIYGASSRATGIP 60
 QY 81 HRFSGSGGDTFTLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKRTVAAPSVFIF 140
 Db 61 DRFSGSGGDTFTLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKRTVAAPSVFIF 120

QY 141 PPS 143
 Db 121 PPS 123

Search completed: April 5, 2004, 13:44:09
 Job time : 12.824 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 12.1827 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-2
Perfect score: 788
Sequence: 1 MDWTRILFLVAAATGTHAQ.....MTVSSASTKGPSVFPLGSR 150
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	580.5	73.7	171	2 S23623	Ig heavy chain V r
2	517.5	65.7	136	2 S31600	Ig heavy chain V r
3	513.5	65.2	135	2 S49530	anti-Sm antibody V
4	508	64.5	627	2 S14683	Ig mu chain precu
5	503	63.8	160	2 PLO105	anti-PK2 erythrocy
6	480.5	61.0	132	2 S31596	Ig heavy chain V r
7	476	60.4	148	2 S29257	Ig heavy chain V r
8	472	59.9	117	2 S18551	Ig heavy chain V r
9	469	59.5	117	2 S31680	Ig heavy chain V r
10	464	58.9	117	1 HVHU35	Ig heavy chain pre
11	455	57.7	142	2 S19245	Ig heavy chain pre
12	452	57.4	117	2 S18553	Ig heavy chain V r
13	450.5	57.2	138	2 PN0538	Ig heavy chain V r
14	449.5	57.0	143	1 ELHUND	Ig heavy chain pre
15	448	56.9	117	2 S18552	Ig heavy chain V r
16	446	56.6	117	1 HVHUHG	Ig heavy chain pre
17	446	56.6	131	2 S21924	Ig heavy chain V r
18	446	56.6	151	2 PLO011	Ig heavy chain pre
19	444	56.3	134	2 S21916	Ig heavy chain V r
20	444	56.3	142	2 A32483	Ig heavy chain V r
21	443	56.2	98	2 S26911	Ig heavy chain V r
22	440.5	55.9	469	2 S37483	Ig gamma-2a chain
23	435.5	55.3	474	1 G2M811	Ig gamma-2b chain
24	432	54.8	117	2 PT0371	Ig gamma chain pre
25	429.5	54.5	137	2 C41287	Ig heavy chain pre
26	423.5	53.7	150	2 PN0444	Ig heavy chain V r
27	422.5	53.6	475	2 S01321	Ig gamma-2b chain
28	421.5	53.5	141	2 JL0076	Ig heavy chain pre
29	420	53.3	111	2 S21925	Ig heavy chain V r

Ig heavy chain pre
Ig heavy chain V r
Ig gamma chain (WM)
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V-1
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V-1
Ig heavy chain V r
Ig heavy chain pre
Ig heavy chain V r
Ig gamma chain - m

ALIGNMENTS

RESULT 1

S23623
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R:Oleee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23623
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 580.5; DB 2; Length 171;
Best Local Similarity 72.4%; Pred. No. 1.9e-41;
Matches 113; Conservative 10; Mismatches 24; Indels 9; Gaps 1;
Qy 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVYKFGASVKVSGYTLTLPVHWGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVYKFGASVKVSGYTLTLPVHWGQAP 60
Qy 61 GKGLWVGSDPESGESIYAREFGQSVTMTADTSTDIAYNELSSLSDDTAVYCAV--- 117
Db 61 GQGLEWNGWINPNSGGTGYGQKFGQVTLTRDTSTIAYNELSRLTSDDTAVYCAIEYF 120
Qy 118 -----PDPAFDIWGQTMVTVSSASTKGPSVFPL 147
Db 121 YDGSDLKPSDVFIDWGQTMVTVSSASTKGPSVFPL 156

RESULT 2

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C. Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585
A:Accession: S31600
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 517.5; DB 2; Length 136;
Best Local Similarity 74.3%; Pred. No. 2.7e-36;
Matches 101; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAT 60

QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDP 120
DB 61 GQGLEWGWNPNSGNTGYAQRFGVTRTSTISATYMELSLRSEDATVYYCA-RWR 119

QY 121 DAFDINGQGTMTVSS 136
DB 120 DAFDINGQGTMTVSS 135

RESULT 3
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <NAH>
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID:G560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 513.5; DB 2; Length 135;
Best Local Similarity 73.5%; Pred. No. 5.8e-36;
Matches 100; Conservative 11; Mismatches 24; Indels 1; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60

QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDP 120
DB 61 GQGLEWGWNPNSGNTGYAQRFGVTRTSTISATYMELSLRSDDTAVYYCA-RAR 119

QY 121 DAFDINGQGTMTVSS 136
DB 120 TGNYMGQGLTVTSS 135

RESULT 4
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nusenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FSI>
A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <NAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 64.5%; Score 508; DB 2; Length 627;
Best Local Similarity 81.2%; Pred. No. 8.5e-35;
Matches 101; Conservative 17; Mismatches 31; Indels 16; Gaps 2;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60

QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA---- 116
DB 61 GQGLEWGWNPNSGNTGYAQRFGVTRTSTISATYMELSLRSEDATVYYCAKTGI 120

QY 117 -----VPDPAF-----DIWQGTMTVSSASTKPSVPPLGS 149
DB 121 LGPVSSGMYNSDYVYGVMDVWGQGTITVTVSSGSASAPTLFPLVS 165

RESULT 5
P10105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C:Accession: P10105
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: P10106; MUID:89235583; PMID:2541221
A:Accession: P10105
A:Molecule type: mRNA
A:Residues: 1-160 <SIL>
A:Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blo
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; hemagglutinin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:49-54/Region: complementarity-determining 1
F:69-84/Region: complementarity-determining 2
F:118-131/Domain: D region <DRG>
F:132-144/Domain: J4 segment <JSG>
F:145-160/Domain: C region <CRG>

Query Match 63.8%; Score 503; DB 2; Length 160;
Best Local Similarity 63.4%; Pred. No. 5.2e-35;
Matches 102; Conservative 12; Mismatches 31; Indels 16; Gaps 3;

QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGVYTLTLPVHWGQAP 60

QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA-VP- 118
DB 61 GQGLEWGWNPNSGNTGYAQRFGVTRTSTISATYMELSLRSDDTAVYYCARPG 120

QY 119 -----DPDAFDINGQGTMTVSSASTKPSVPPLGS 149
DB 121 YCSGGGCVRGD-----DYWGQGTITVTVSSGSASAPTLFPLVS 157

RESULT 6
S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 61.0%; Score 480.5; DB 2; Length 132;
Best Local Similarity 69.9%; Pred. No. 3.2e-33;
Matches 95; Conservative 11; Mismatches 25; Indels 5; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAT 60
QY 61 GKLEWVGSPDPESGSIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYCAVDPD 120
DB 61 GQGLEWGWNPNSGNTGYAQKFGQVTRTSTISATYMELSLRSDDTAVYCAVDPD 116
QY 121 DAFDINGQGTMTVSS 136
DB 117 -KAPANGQGTMTVSS 131
RESULT 7
S29257
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouhane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment e
A:Reference number: S29257; MUID:92362614; PMID:1499555
A:Accession: S29257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:S4203; NID:G253699; PIDN:AAB22940.1; PID:G253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 60.4%; Score 476; DB 2; Length 148;
Best Local Similarity 62.2%; Pred. No. 8.5e-33;
Matches 92; Conservative 14; Mismatches 30; Indels 12; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTFAMVAHWVQAP 60
QY 61 GKLEWVGSPDPESGSIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYCAVDPD 116
DB 61 GQGLEWGWNPNSGNTGYAQKFGQVTRTSTISATYMEVRLSRSDDTAVYCAVDPD 116
QY 117 -----VPDPAFDINGQGTMTVSS 136
DB 121 INMVRGLITTPPWFDSWGQGLIVSS 148
RESULT 8
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S21625
R:Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62166; NID:G37831; PIDN:CAA44016.1; PID:G37832

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:G32552; PIDN:CAA42225.1; PID:G32553
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 59.8%; Score 472; DB 2; Length 117;
Best Local Similarity 77.6%; Pred. No. 1.4e-32;
Matches 90; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTFGYNHWVQAP 60
QY 61 GKLEWVGSPDPESGSIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYCA 116
DB 61 GQGLEWGWNPNSGNTGYAQKFGQVTRTSTISATYMELSLRSDDTAVYCA 116
RESULT 9
S31680
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31680
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31680
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <CUI>
A:Cross-references: EMBL:Z14213; NID:G37795; PIDN:CAA78582.1; PID:G37796
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 59.5%; Score 469; DB 2; Length 117;
Best Local Similarity 75.9%; Pred. No. 2.5e-32;
Matches 88; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTLTLPVHWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVGYTFYSYNHWVQAP 60
QY 61 GKLEWVGSPDPESGSIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYCA 116
DB 61 GQGLEWGWNPNSGNTGYAQKFGQVTRTSTISATYMELSLRSDDTAVYCA 116
RESULT 10
HVHU35
Ig heavy chain precursor V region (V35) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C:Accession: S00476; S34013
R:Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh
EMBO J. 7, 1047-1051, 1988
A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain 1
A:Reference number: S00476; MUID:88296408; PMID:2841108

```
A:Accession: S00476
A:Molecule type: DNA
A:Residues: 1-117 <MATS>
A:Cross-references: EMBL:X07448; NID:g33104; PIDN:CA56703.1; PID:g6002173
A:Note: the authors translated the codon AGT for residue 89 as Met
R:Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34013
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 20-116 <MAR>
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:l128528; OMIM:l47070
A:Map position: 14q32.33-14q32.33
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 464; DB 1; Length 117;
Best Local Similarity 75.9%; Pred. No. 6.6e-32;
Matches 88; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60

Qy 61 GKLEWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
Db 61 GQGLEWGRINPNSGGTNYAKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCA 116

RESULT 11
SI9245
Ig heavy chain precursor V region (10P1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: SI9245
R:Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
EMBO J. 11, 603-609, 1992
A:Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure
A:Reference number: SI9245; MUID:92164649; PMID:1537339
A:Accession: SI9245
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-142 <KIR>
A:Cross-references: EMBL:X59906; NID:g37791; PIDN:CAA42547.1; PID:g37792
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 57.7%; Score 455; DB 2; Length 142;
Best Local Similarity 60.6%; Pred. No. 4.6e-31;
Matches 86; Conservative 19; Mismatches 31; Indels 6; Gaps 1;

Qy 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60

Qy 61 GKLEWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA --- 116
Db 61 GQGLEWGWINTNTGNFTFAQGTFRVPSLDSVSTAYLQISLRAEDTAVYYCARAYT 120

Qy 117 --VPPDAFDIWGGTWTYSS 136
Db 121 LMMTAVTHFDWGGQGLTVYSS 142
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RESULT 12
SI8553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: SI8553; S26916
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Inai, T.; Yokoyama, K.; Soeda, E.;
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c
A:Reference number: SI8551; MUID:92037524; PMID:1935893
A:Accession: SI8553
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62109
R:Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26916
A:Molecule type: DNA
A:Residues: 20-117 <TOM>
A:Cross-references: EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID:g32872
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 57.4%; Score 452; DB 2; Length 117;
Best Local Similarity 73.3%; Pred. No. 6.6e-31;
Matches 85; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60

Qy 61 GKLEWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
Db 61 GQLEWGMWAGNAGNTKYSQKFGRTITRDTASTAYMELSLRSDDTAVYYCA 116

RESULT 13
PN0538
Ig heavy chain V region (clone LUNm03) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C:Accession: PN0538
R:Avila, M.A.; Vazquez, J.; Danielsson, L.; de Cossio, M.E.F.; Borrebaeck, C.A.K.
Gene 127, 273-274, 1993
A:Title: Sequence determination of variable region genes of two human monoclonal antibo
A:Reference number: PN0535; MUID:93273246; PMID:8500770
A:Accession: PN0538
A:Molecule type: DNA
A:Residues: 1-138 <AVI>
A:Cross-references: GB:M97804; NID:g185373; PIDN:AAB18935.1; PID:g1669777
A:Note: the authors translated the codon CCA for residue 75 as Ser, GCC for residue 79
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.2%; Score 450.5; DB 2; Length 138;
Best Local Similarity 65.2%; Pred. No. 1.1e-30;
Matches 90; Conservative 10; Mismatches 23; Indels 15; Gaps 1;

Qy 20 QVLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAPKGLVWVSGDPSGSIY 79
Db 1 QVHLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVDRPLGKLEWNGDFPEGGSIY 60

Qy 80 AREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPD-----DAFD 124
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Db 61 AQKQGRVTMTDPTDTSLELSVRSEDATVYVCVTGPPRLSELALFGVWKIRGPPD 120
QY 125 IWGQGTMTVVSASTKGP 142
Db 121 IWGQGTMTVVSASTKGP 138

RESULT 14
ELHUND
Ig heavy chain precursor V-I region (Nd) - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C:Accession: A93933; A02026
R:Kerten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: A93933
A:Molecule type: mRNA
A:Residues: 1-143 <KEN>
R:Benrich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Contents: annotation: partial sequence
A:Note: this epsilon chain was isolated from a myeloma protein
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
F:30-113/Domain: immunoglobulin homology <IMM>
F:16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F:37-111/Disulfide bonds: #status experimental

Query Match 57.0%; Score 449.5; DB 1; Length 143;
Best Local Similarity 61.2%; Pred. No. 1.3e-30;
Matches 90; Conservative 12; Mismatches 30; Indels 15; Gaps 2;

QY 1 MDWTWRIILFLVAAATGTHAQVOLVQSGAEVKPKGASVKVCKVSGYTLTLPVHVWGQAP 60
Db 1 MDWT---FLVAAATRVHSQTOLVQSGAEVKPKGASVRVCKVSGYTFIDSYIHWRQAP 56

QY 61 GKGLEWVGSDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAYVYCAVPDP 120
Db 57 GHGLEWVGWNPNSGGTNYAPRFQGRVTMTDRDASFSTAYMDLRLSLRSDSAVFYCAKSDP 116

QY 121 -----DAFDIWGQGTMTVSS 136
Db 117 FMSDYNYFDYSYTLVDWGQGTITVSS 143

RESULT 15
SI8552
Ig heavy chain V region precursor (VI-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: SI8552
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: SI8551; MUID:92037524; PMID:1935893
A:Accession: SI8552
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62107; NID:g37833; PIDN:CAA44017.1; PID:g37834
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3) #status predicted <VAT>
F:34-117/Domain: immunoglobulin homology <IMM>

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Query Match 56.9%; Score 448; DB 2; Length 117;
Best Local Similarity 73.3%; Pred. No. 1.4e-30;
Matches 85; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

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QY 1 MDWTWRIILFLVAAATGTHAQVOLVQSGAEVKPKGASVKVCKVSGYTLTLPVHVWGQAP 60
Db 1 MDWTWRIILFLVAAATGTHAQVOLVQSGAEVKPKGASVKVCKVSGYTFISYAMHWVRQAP 60

QY 61 GKGLEWVGSDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAYVYCA 116
Db 61 GORLEWVGMSNAGNGNTKYSQEFQGRVTITRDTASTAYMELSLRSEDMAVYCA 116

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Search completed: April 5, 2004, 13:43:01
Job time : 12.1827 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:10:21 ; Search time 6.85279 Seconds
(without alignments)
1139.758 Million cell updates/sec

Title: US-10-044-569B-2
Perfect score: 788
Sequence: 1 MDWTRILFLVAAATGTHAQ.....MTVSSASTKGPSVPFLQSR 150

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464	58.9	117	1 HV1G HUMAN	P23083 homo sapien
2	456.5	57.9	147	1 HV1C HUMAN	P01744 homo sapien
3	446	56.6	117	1 HV1B HUMAN	P01743 homo sapien
4	414.5	52.6	139	1 HV07 MOUSE	P01751 mus musculus
5	406.5	51.6	137	1 HV11 MOUSE	P01755 mus musculus
6	396	50.3	138	1 HV11 MOUSE	P03980 mus musculus
7	374	47.5	117	1 HV05 MOUSE	P01750 mus musculus
8	374	47.5	117	1 HV09 MOUSE	P01753 mus musculus
9	373	47.3	136	1 HV15 MOUSE	P01759 mus musculus
10	369	46.8	140	1 HV02 MOUSE	P01746 mus musculus
11	364	46.2	117	1 HV04 MOUSE	P01748 mus musculus
12	360	45.7	117	1 HV49 MOUSE	P06328 mus musculus
13	356	45.2	117	1 HV14 MOUSE	P01758 mus musculus
14	355	45.1	117	1 HV10 MOUSE	P01754 mus musculus
15	354	44.9	117	1 HV05 MOUSE	P01749 mus musculus
16	351	44.5	117	1 HV1A HUMAN	P01742 homo sapien
17	350	44.4	117	1 HV52 MOUSE	P06327 mus musculus
18	346.5	44.0	118	1 HV51 MOUSE	P06330 mus musculus
19	346	43.9	117	1 HV13 MOUSE	P01756 mus musculus
20	345	43.8	117	1 HV13 MOUSE	P01757 mus musculus
21	338.5	43.0	120	1 HV50 MOUSE	P06329 mus musculus
22	332.5	42.2	114	1 HV00 MOUSE	P01741 mus musculus
23	326	41.4	120	1 HV03 MOUSE	P01747 mus musculus
24	318	40.4	121	1 HV01 MOUSE	P01745 mus musculus
25	313.5	39.8	120	1 HV1H HUMAN	P80421 homo sapien
26	313	39.7	125	1 HV1F HUMAN	P06326 homo sapien
27	306.5	38.9	122	1 HV3G HUMAN	P01768 homo sapien
28	305	38.7	121	1 HV3J HUMAN	P01771 homo sapien
29	301.5	38.3	124	1 HV1E HUMAN	P01761 homo sapien
30	293	37.2	119	1 HV3I HUMAN	P01770 homo sapien
31	291.5	37.0	136	1 HV16 MOUSE	P01783 mus musculus
32	290.5	36.9	124	1 HV1D HUMAN	P01760 homo sapien
33	290	36.8	142	1 HV01 RAT	P01805 rattus norv

34	286.5	36.4	114	1 HV01 CANFA	P01784 canis famil
35	284.5	36.1	122	1 HV3H HUMAN	P01769 homo sapien
36	284	36.0	119	1 HV3L HUMAN	P01773 homo sapien
37	280.5	35.6	117	1 HV03 CARAU	P19180 carassius a
38	277.5	35.2	120	1 HV3U HUMAN	P01782 homo sapien
39	276	35.0	117	1 HV3C HUMAN	P01784 homo sapien
40	275	34.9	115	1 HV3D HUMAN	P01785 homo sapien
41	274.5	34.8	114	1 HV3B HUMAN	P01783 homo sapien
42	274.5	34.8	116	1 HV3T HUMAN	P01781 homo sapien
43	272.5	34.6	126	1 HV3K HUMAN	P01772 homo sapien
44	272	34.5	117	1 HV01 CAICR	P01813 caiman croc
45	271.5	34.5	119	1 HV38 MOUSE	P01808 mus musculus

ALIGNMENTS

RESULT 1					
HV1G HUMAN					
ID	HV1G HUMAN	STANDARD;	PRT;	117 AA.	
AC	P23083;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	IG heavy chain V-I region V35 precursor.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88296408; PubMed=2841108;				
RA	Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,				
RA	Ohno H., Fukuhara S., Honjo T.;				
RT	"Dispersed localization of D segments in the human immunoglobulin heavy-chain locus.";				
RL	EMBO J. 7:1047-1051(1988).				
CC	!- SIMILARITY: Contains 1 immunoglobulin-like domain.				
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CC	EMBL; X07448; -; NOT_ANNOTATED_CDS.				
DR	PIR; S00476; HVH035.				
DR	HSSP; P01772; 2FB4.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003596; IG_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL 1 19				
FT	CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.				
FT	DOMAIN 20 >117 IG-LIKE.				
FT	NON_TER 117 117				
SQ	SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;				
Query Match 58.9%; Score 464; DB 1; Length 117;					
Best Local Similarity 75.9%; Pred. No. 1.5e-36;					
Matches 88; Conservative 8; Mismatches 20; Indels 0; Gaps 0;					
Oy	1 MDWTRILFLVAAATGTHAQVOLVQSGAEYKPKGASVKVSGYGLTELPEVHWGQAP 60				
DB	1 MDWTRILFLVAAATGTHAQVOLVQSGAEYKPKGASVKVSGYGLTELPEVHWGQAP 60				


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RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00529; AAA38170.1; -.
DR PIR: A0809; MMS18.
DR FDB: 1A6W; 27-MAY-98.
DR FDB: 1A6W; 15-JUL-98.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 62 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 52.6%; Score 414.5; DB 1; Length 139;
Best Local Similarity 57.6%; Pred. No. 7.5e-32;
Matches 80; Conservative 17; Mismatches 39; Indels 3; Gaps 1;

Qy 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKSVKSGYTLTELPVHWVGQAP 60
Db 1 MGWSCIMFLAATATGVSQVQLQPGAEVYKPGASVKLSCKASGYTFTSYMHWVKQRP 60

Qy 61 GKGLWVGSGFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVPD- 119
Db 61 GRGLEWIGRIDPNSGGTKYNEFKSKATLTVDPKPSSTAYMQLSLTSDESAVYCYDY 120

Qy 120 --PDADFIDWGQGTMTVSS 136
Db 121 YGSSYFDYWGQGTTLTVSS 139

RESULT 5
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00539; AAA38172.1; -.
DR PIR: A02038; G2MS43.
DR HSP: P01810; 2FBU.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 62 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 51.6%; Score 406.5; DB 1; Length 137;
Best Local Similarity 57.7%; Pred. No. 4.1e-31;
Matches 79; Conservative 15; Mismatches 42; Indels 1; Gaps 1;

Qy 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKSVKSGYTLTELPVHWVGQAP 60
Db 1 MGWSCIMFLAATATGVSQVQLQPGAEVYKPGASVKLSCKASGYTFTSYLMHWVQRP 60

Qy 61 GKGLWVGSGFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCA-VPD 119
Db 61 GRGLEWIGRIDPNSGGTKYNEFKSKATLTVDPKPSSTAYMQLSLTSDESAVYCYRL 120

Qy 120 PDADFIDWGQGTMTVSS 136
Db 121 GRYFDYWGQGTTLTVSS 137

RESULT 6
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.B., Blattner F.R., Mushinski J.F.,

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RA Tucker P.W.:
RT "Illegitimate recombination generates a class switch from C mu to C
RL delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
DR PIR; AC2033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 74815734C6907B8E CRC64;

Query Match 50.3%; Score 396; DB 1; Length 138;
Best Local Similarity 55.1%; Pred. No. 4e-30;
Matches 76; Conservative 20; Mismatches 40; Indels 2; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVGYTLTLPVHWGQAP 60
DB 1 MGWSYILFLVATATDVHSHVQLQPGAEVLKPGASVKVSKAGHTFTYHWHVKQRP 60

QY 61 KGLEWVGSDPPSGESIYAREFGQSVTMTADTSTDIAYNELSLRSDDTAVYCAVPP 120
DB 61 GQGLEWIGEINPDGRSNYNEKFKATLTVDKSSSTAYMQLSSLTPPEFAVYVCARSDG 120

QY 121 --DAFDWGGTVMTVSS 136
DB 121 YDWFVYWGQGLTVTFSA 138

RESULT 7
HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637 (1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; D90809; HVM561.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 47.5%; Score 374; DB 1; Length 117;
Best Local Similarity 59.5%; Pred. No. 3.7e-28;
Matches 69; Conservative 16; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVGYTLTLPVHWGQAP 60
DB 1 MGWSYILFLVATATDVHSHVQLQPGAEVLKPGASVKVSKAGHTFTYHWHVKQRP 60

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FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851PCA8C CRC64;

Query Match 47.5%; Score 374; DB 1; Length 117;
Best Local Similarity 59.0%; Pred. No. 3.7e-28;
Matches 69; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVGYTLTLPVHWGQAP 60
DB 1 MGWSYILFLVATATDVHSHVQLQPGAEVLKPGASVKVSKAGHTFTYHWHVKQRP 60

QY 61 KGLEWVGSDPPSGESIYAREFGQSVTMTADTSTDIAYNELSLRSDDTAVYCAV 117
DB 61 GQGLEWIGRIHPSDSDTNNQKFKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAI 117

RESULT 8
HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; F11271;
DT 21-JUL-1986 (Rel. 01, Created)
DE 01-JUL-1989 (Rel. 11, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637 (1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; D90809; HVM561.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 47.5%; Score 374; DB 1; Length 117;
Best Local Similarity 59.5%; Pred. No. 3.7e-28;
Matches 69; Conservative 16; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVGYTLTLPVHWGQAP 60
DB 1 MGWSYILFLVATATDVHSHVQLQPGAEVLKPGASVKVSKAGHTFTYHWHVKQRP 60

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QY 61 GKLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYCA 116
DB 61 GKLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSTAYMQLHSUTSDESAVYCA 116

RESULT 9
HV15 MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DE 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00494; AAA38130.1; -.
DR PIR; A02042; HVM5B1.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT DOMAIN 20 135 IG-LIKE.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6D3F35E CRC64;

Query Match 47.3%; Score 373; DB 1; Length 136;
Best Local Similarity 52.9%; Pred. No. 5.5e-28;
Matches 72; Conservative 20; Mismatches 44; Indels 0; Gaps 0;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWGQAP 60
DB 1 MGWSCIPLVATATGVHSQVQLQSGPEVVRPGVSVKISCKSGYTFDAMHWKQSH 60

QY 61 GKLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
DB 61 AKSLEWIGVISTYNGTSTNOKFKGATMTVDKSSSTVHMLARLTSDEDSANLYCARYG 120

QY 121 DAFDINGQGTMTVSS 136
DB 121 NYFDYWGQGTTLTVSS 136

RESULT 10
HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HVM5G7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DASCE8 CRC64;

Query Match 46.8%; Score 369; DB 1; Length 140;
Best Local Similarity 50.0%; Pred. No. 1.3e-27;
Matches 70; Conservative 25; Mismatches 41; Indels 4; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWGQAP 60
DB 1 MGWSFIFLLSVTAGVHSEVQLQSGAEIVRAGSSVQKMSCKASGYTFTSYGINWYKQP 60

QY 61 GKLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYCA--- 116
DB 61 GQLEWIGVINGVINGVINGVINGVINGVINGVINGVINGVINGVINGVINGVINGV 120

QY 117 VPDPDAFDINGQGTMTVSS 136
DB 121 YGGSYDFDYWGQGTPLTVSS 140

RESULT 11
HV04 MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; A02030; HVS23.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 46.2%; Score 364; *DB 1; Length 117;
Best Local Similarity 58.6%; Pred. No. 3.2e-27;
Matches 68; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1 MDMTWRILFLVAATGTHAQVQLVQSGAEVKGASVKVSKVGYTLTLPVHWYQAP 60
DB 1 MGNSCIILFLVAANGVHSVQLQPGTGLVKGASVKLSCKASGYTFTSYNHWYKQRP 60
QY 61 GKLEWVGSFDPSEGSIIYAREFGQSVTMTADTSTDIAYMELSLSDTAVYCA 116
DB 61 GQGLEWIGNPFGNGTNYNEKPKSKVTLTVKSSSTAYTQLSSLTSEDSAVYCA 116

RESULT 12
HV49 MOUSE
ID HV49 MOUSE STANDARD; PRT; 117 AA.
AC P6328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
CC EMBL; M13786; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.

RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; A02030; HVS23.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 45.7%; Score 360; DB 1; Length 117;
Best Local Similarity 57.4%; Pred. No. 7.6e-27;
Matches 66; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 1 MDMTWRILFLVAATGTHAQVQLVQSGAEVKGASVKVSKVGYTLTLPVHWYQAP 60
DB 1 MGNSCIILFLVAATGTHAQVQLVQSGAEVKGASVKVSKVGYTLTLPVHWYKQRP 60
QY 61 GKLEWVGSFDPSEGSIIYAREFGQSVTMTADTSTDIAYMELSLSDTAVYCA 115
DB 61 GRGLEWIGNIDPNSGGTKYNEKPKSKATLVDPKSPSTAYMQLSLSLTSEDSAVYCA 115

RESULT 13
HV14 MOUSE
ID HV14 MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00488; AAA38519.1; -.
DR PIR; A02041; HVM58A.
DR HSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

```

```
Query Match 45.2%; Score 356; DB 1; Length 117;
Best Local Similarity 55.4%; Pred. No. 1.8e-26;
Matches 64; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSKVSGYVTLTLPVHWVQGP 60
DB 1 MGWSWIFLLSCTAGVHSVQLQSGPELVKPGASVKISCKASGYTFTDYNHWVQKSH 60

QY 61 GKGLWVSGDPESGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
DB 61 GKSLWIGIYIPYNGGTGYNQKPKATLTVDNSSSTAYMELSSLTSEDSAVYYCA 116

RESULT 14
HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00533; AAA38602.1; -
CC PIR; C90809; HVMS45.
CC HSP; P01810; 2PBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Igh-like.
CC InterPro; IPR003596; Igh_v.
CC Pfam; PF00047; Igh; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 117 117
CC SEQUENCE 117 AA; 12921 MW; D37D8A3F543E996 CRC64;

Query Match 45.1%; Score 355; DB 1; Length 117;
Best Local Similarity 57.8%; Pred. No. 2.2e-26;
Matches 67; Conservative 15; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSKVSGYVTLTLPVHWVQGP 60
DB 1 MGWSWIFLLSCTAGVHSVQLQSGPELVKPGASVKISCKASGYTFTDYNHWVQKSH 60

QY 61 GKGLWVSGDPESGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
DB 61 GKSLWIGIYIPYNGGTGYNQKPKATLTVDNSSSTAYMELSSLTSEDSAVYYCA 116

RESULT 15
HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00536; AAA38605.1; -
CC PIR; A02031; HVMS3.
CC HSP; P01810; 2PBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Igh-like.
CC InterPro; IPR003596; Igh_v.
CC Pfam; PF00047; Igh; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 117 117
CC SEQUENCE 117 AA; 427C861C53975EDC CRC64;

Query Match 44.9%; Score 354; DB 1; Length 117;
Best Local Similarity 56.9%; Pred. No. 2.7e-26;
Matches 66; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPKGASVKVSKVSGYVTLTLPVHWVQGP 60
DB 1 MGWSWIFLLVATGTHVHSVQLQSGPELVKPGASVKISCKASGYTFTSWMDVWVQRP 60

QY 61 GKGLWVSGDPESGSIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCA 116
DB 61 GGLWIGIYIPSDSETHYQKPKATLTVDKSSSTAYMQLSLTSEDSAVYYCA 116
```

Search completed: April 5, 2004, 13:24:55
Job time : 7.85279 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:24:21 ; Search time 31.9797 Seconds
(without alignments)
1479.931 Million cell updates/sec

Title: US-10-044-569B-2

Perfect score: 788

Sequence: 1 MDWTRILFLVAAATGTHAQ.....MTVSSASTKGPSVFPPLGSR 150

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	788	100.0	150	4	Q9Y298 homo sapien
2	520.5	66.1	469	4	Q727P5
3	510	64.7	614	4	Q9SGA6
4	478.5	60.7	500	4	Q9BRV0
5	467	59.3	497	4	Q8WY24
6	466	59.1	473	11	Q9D8L4
7	464	58.9	157	4	Q95978
8	461.5	58.6	159	4	Q96QSO
9	445.5	56.5	613	11	Q8VCX7
10	445	56.5	168	11	Q8VDC9
11	443.5	56.3	482	11	Q91LA6
12	443.5	55.3	278	11	Q91KI1
13	435.5	55.1	463	11	Q91LC4
14	434.5	54.8	473	11	Q91L25
15	431.5	54.4	470	11	Q7TMK1
16	429				

17	428	54.3	468	11	Q99L31	Q99L31 mus musculu
18	425	53.9	125	4	Q9UL95	Q9UL95 homo sapien
19	421.5	53.5	124	4	Q9UL92	Q9UL92 homo sapien
20	421	53.4	480	11	Q8KOZ4	Q8KOZ4 mus musculu
21	421	53.4	481	11	Q91WT1	Q91WT1 mus musculu
22	418.5	53.1	488	11	Q91WR1	Q91WR1 mus musculu
23	412.5	52.3	496	4	Q96DK0	Q96DK0 homo sapien
24	409.5	52.0	481	11	Q8VCV5	Q8VCV5 mus musculu
25	409.5	52.0	488	11	Q8KOF2	Q8KOF2 mus musculu
26	409	51.9	474	11	Q833H6	Q833H6 mus musculu
27	407	51.6	119	4	Q9UL94	Q9UL94 homo sapien
28	407	51.6	614	11	Q7TMT6	Q7TMT6 mus musculu
29	406	51.5	481	11	Q91WT3	Q91WT3 mus musculu
30	405	51.4	489	11	Q8VCX4	Q8VCX4 mus musculu
31	398.5	50.6	143	11	Q924R0	Q924R0 mus musculu
32	398.5	50.6	145	11	Q924R4	Q924R4 mus musculu
33	394.5	50.1	145	11	Q924R1	Q924R1 mus musculu
34	393.5	49.9	143	11	Q924Q5	Q924Q5 mus musculu
35	392.5	49.8	143	11	Q91VA2	Q91VA2 mus musculu
36	392.5	49.8	143	11	Q924R7	Q924R7 mus musculu
37	391	49.6	142	11	Q924Q1	Q924Q1 mus musculu
38	390.5	49.6	143	11	Q91V67	Q91V67 mus musculu
39	390.5	49.6	145	11	Q924P7	Q924P7 mus musculu
40	388.5	49.3	145	11	Q924Q9	Q924Q9 mus musculu
41	388.5	49.3	145	11	Q924Q7	Q924Q7 mus musculu
42	388	49.2	146	11	Q924Q3	Q924Q3 mus musculu
43	387.5	49.2	145	11	Q924R3	Q924R3 mus musculu
44	386.5	49.0	145	11	Q924Q6	Q924Q6 mus musculu
45	385.5	48.9	137	11	Q924R6	Q924R6 mus musculu

ALIGNMENTS

RESULT 1

Q9Y298 ID Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IGG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL. 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 563D164AB2802D5 CRC64;

Query Match 100.0%; Score 788; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 5,9e-66;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A33CC6D9 CRC64;

Query Match 60.7%; Score 478.5; DB 4; Length 500;
Best Local Similarity 60.8%; Pred. No. 2.5e-36;
Matches 96; Conservative 13; Mismatches 38; Indels 11; Gaps 2;

QY 1 MDWTWRLFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MDMTWSILFLVAAATGAQSQVHLVQSGAEVMPGASRVSKTSGYAFHTYSIIWVRQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCA--- 116
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GQGLEWNGWISPSDDNTRFAKPGQGRVTLTDTSTVTVMELSLRSDDTAVYCCARRYC 120

QY 117 ---VPDPAF---DIWGGQTMVTSSASTKGPSVFPPL 147
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 SYSSCCNDYYMYDMVNGKTTVTSSASPTSPKVFPL 158

RESULT 5
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT "Identification and characterization of SNC66, a Ig-like gene which is
sub-regulated in colorectal cancer."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL: AF283666; AAL36987.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 59.3%; Score 467; DB 4; Length 497;
Best Local Similarity 57.4%; Pred. No. 2.9e-35;
Matches 89; Conservative 24; Mismatches 34; Indels 8; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MDMTWRLFLVAAATGAHSEQLVQSGAEVTKPGASVKVSCKASGYTFYADINWVRQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVDP- 119
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GQGLEWNGWNPQNTGNTPEAKFQGRITTSRDTSTINTAYMVLSSLTSDSAIFYCARGNL 120

QY 120 -----PDADFDTWGGQTMVTSSASTKGPSVFPPL 147
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 RGRGFGYWNFDPWGHGTLTVTSASPTSPKVFPL 155

RESULT 6

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Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE I81060009R1k protein.
GN IGH-1 OR I81060009R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancraeas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK007918; BAB325349.1; -.
DR PIR: S26746; S26746.
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 59.1%; Score 466; DB 11; Length 473;
Best Local Similarity 57.7%; Pred. No. 3.4e-35;
Matches 86; Conservative 23; Mismatches 38; Indels 2; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MEWSWFLFLSVTAGVHCQVQLKQSGAEVLPKPGASVKISCKASGYTFYDINWVRQAP 60
QY 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCAVP-- 118
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GQGLEWIGKIGPGSGSYVNEKFGKATLTADKSSSTAYVQLSSLTSDSAVYFCARSGY 120

QY 119 DPDAFDITWGGQTMVTSSASTKGPSVFPPL 147
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 DYDFWYWGQGTTLTVSAKTTAPSVYPL 149

RESULT 7
Q95978 PRELIMINARY; PRT; 157 AA.
AC Q95978;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

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DE VH1 protein precursor (Fragment).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularity Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes.";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ005570; CAA06599.1; -
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR SIGNAL.
KW SIGNAL.
FT 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;

Query Match 58.9%; Score 464; DB 4; Length 157;
Best Local Similarity 59.6%; Pred. No. 1.3e-35;
Matches 90; Conservative 17; Mismatches 40; Indels 4; Gaps 1;

Qy 1 MDWTWRILFLVAATGTHAQVLVQSGAEVKKPKGASVKVSKYGYTLTLPVHWGQAP 60
Db 1 MDWTWRVFCLLAVPGVHSQVLVQSGAEVKKPKGASVKVSKYGYTLTLPVHWGQAP 60
Qy 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVVYCA- 116
Db 61 GKGLEWVGGIGPGVGSTMCRAEKQGLTMTNTSTITVYMELSLRLAFEDTAVVFCGGR 120
Qy 117 VPDPDAFDWQGTMTVSSASTKGPSVFPL 147
Db 121 WRSGNYNGHWGQGTPTVTVSSSTKGPSVFPL 151

Query Match 56.5%; Score 445.5; DB 11; Length 613;
Best Local Similarity 57.3%; Pred. No. 3.9e-33;
Matches 86; Conservative 20; Mismatches 43; Indels 1; Gaps 1;

Qy 1 MDWTWRILFLVAATGTHAQVLVQSGAEVKKPKGASVKVSKYGYTLTLPVHWGQAP 60
Db 1 MEWTWVFLFLSVTAGVHSQVLQSGAELMKPGASVKISKATGYTFSSYIEWVKQRP 60
Qy 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVVYCAVP-D 119
Db 61 GHGLEWIGEILPGSGSTNYNEKFKGATFTADTSSNTAYMQLSLTSDSAVYICARL 120
Qy 120 PDAFDWQGTMTVSSASTKGPSVFPLGS 149
Db 121 RWPFDVWGAGTTVTVSSSQSPFNVPFLVS 150

RESULT 10
Q8VDC9
ID Q8VDC9 PRELIMINARY; PRT; 168 AA.
AC Q8VDC9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-MOG 212 variable gamma 2a (fragment).
GN IGG2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Matches 89; Conservative 17; Mismatches 36; Indels 13; Gaps 1;

Qy 1 MDWTWRILFLVAATGTHAQVLVQSGAEVKKPKGASVKVSKYGYTLTLPVHWGQAP 60
Db 1 MDWTWRVFCLLAVPGVHSQVLVQSGAEVKKPKGASVKVSKYGYTFSSYIWNWVQAP 60
Qy 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVVYCAVPDP 120
Db 61 GQGFEMGVNFPSCGSARYSQKFGRLTMTDRTSTVYMDLSRLSDDTAVVFCAREME 120
Qy 121 DAP-----DINGQGTMTVSSASTKGP 142
Db 121 ITFGAVSKGPFYYXGMDVWGQGTITVTVSSHPRPAP 155

RESULT 9
Q8VCX7
ID Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAL18315.1; -
DR MGD; MGI:96448; IGH-6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IGH_MHC.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 56.5%; Score 445.5; DB 11; Length 613;
Best Local Similarity 57.3%; Pred. No. 3.9e-33;
Matches 86; Conservative 20; Mismatches 43; Indels 1; Gaps 1;

Qy 1 MDWTWRILFLVAATGTHAQVLVQSGAEVKKPKGASVKVSKYGYTLTLPVHWGQAP 60
Db 1 MEWTWVFLFLSVTAGVHSQVLQSGAELMKPGASVKISKATGYTFSSYIEWVKQRP 60
Qy 61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVVYCAVP-D 119
Db 61 GHGLEWIGEILPGSGSTNYNEKFKGATFTADTSSNTAYMQLSLTSDSAVYICARL 120
Qy 120 PDAFDWQGTMTVSSASTKGPSVFPLGS 149
Db 121 RWPFDVWGAGTTVTVSSSQSPFNVPFLVS 150

RESULT 10
Q8VDC9
ID Q8VDC9 PRELIMINARY; PRT; 168 AA.
AC Q8VDC9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-MOG 212 variable gamma 2a (fragment).
GN IGG2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c;
RC Chernaiovsky Y;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembi P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ16332; CAC94867.1; -.
DR InterPro; IPR007110; Ig_Like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 168
SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match 56.5%; Score 445; DB 11; Length 168;
Best Local Similarity 55.7%; Pred. No. 8.3e-34;
Matches 83; Conservative 21; Mismatches 43; Indels 2; Gaps 1;

QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
Db 1 MENTWVFLVLSVTAGVHSQVQLQSGAEELKPGASVKCAKTGTFSSYIDWVWQRP 60

QY 61 KGLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
Db 61 GHGLEWIGEILPGSGRTNYNEKFKGKTTFTADTSSNTAVYIQFSSLTSEDSAVYYCANYGS 120

QY 121 DA--FDWVGQGTWVTSSASTKGPSVFPL 147
Db 121 SRWYFDWVGAGTIVTSSTKTTPSVYPL 149

RESULT 11
Q99LA6 PRELIMINARY; PRT; 484 AA.
AC -Q99LA6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034395; AA034395.1; -.
DR PIR; F33932; F33932.
DR HSP; P01810; 2FEJ.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 484 AA; 52567 MW; 8EAE4A9BCF582FA CRC64;

Query Match 56.5%; Score 445; DB 11; Length 484;
Best Local Similarity 52.3%; Pred. No. 3.2e-33;
Matches 79; Conservative 31; Mismatches 37; Indels 4; Gaps 1;

QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034395; AA034395.1; -.
DR PIR; F33932; F33932.
DR HSP; P01810; 2FEJ.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 484 AA; 52567 MW; 8EAE4A9BCF582FA CRC64;

Query Match 56.3%; Score 443.5; DB 11; Length 482;
Best Local Similarity 56.8%; Pred. No. 4.4e-33;
Matches 84; Conservative 20; Mismatches 43; Indels 1; Gaps 1;

QY 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
Db 1 MGWSCIMFLAATATGHSQVQLQSGAEELKPGASVKCAKTGTFSSYIDWVWQRP 60

QY 61 KGLEWVGSFDPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA-VPD 119
Db 61 GRGLEWICRIDPSNGTKYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTREGD 120

QY 120 PDAPFWGQGTWVTSSASTKGPSVFPL 147
Db 120 PDAPFWGQGTWVTSSASTKGPSVFPL 147
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Db 121 YDAMYWGQCTSVTSSEPAEPTIYPL 148
      121 YDAMYWGQCTSVTSSEPAEPTIYPL 148

RESULT 13
Q921KI ID Q921KI PRELIMINARY; PRT; 278 AA.
AC Q921KI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein.
KW
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 55.3%; Score 435.5; DB 11; Length 278;
Best Local Similarity 56.7%; Pred. No. 1.2e-32;
Matches 85; Conservative 18; Mismatches 44; Indels 3; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWVQAP 60
Db 1 MGWNCIILFVATATGVSQVQLQPGAEELVKPGASVKASGYSYFYSYWHHWVQRR 60
QY 61 KGLEWVGSFDPESGESIYAREFOGVSVMYADTSTDIAYMELSLRSDDTAVYCAVP-- 118
Db 61 GQGLEWIGNINPNSGGNYNEKFKGKATLAVDKSSSVTVYMQLSLTSSEDSAVYCTRGV 120
QY 119 -DPADFIWGQGTMTVSSASTKGPSVFPL 147
Db 121 YDDYFVFWGAGTITVSSAKTTAPSVYPL 150

RESULT 14
Q99LC4 ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181006O009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR FPIR; B45837; B45837.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.

SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 55.1%; Score 434.5; DB 11; Length 463;
Best Local Similarity 54.0%; Pred. No. 2.9e-32;
Matches 81; Conservative 25; Mismatches 41; Indels 3; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWVQAP 60
Db 1 MEWIIWIFLISGTAGVHSQVQLQSGAELARPGASVRLSKASGYFTFGVGVSWVKQRT 60
QY 61 KGLEWVGSFDPESGESIYAREFOGVSVMYADTSTDIAYMELSLRSDDTAVYCAVPDP 120
Db 61 GQGLEWGEIYIPGSGNTYSEKFKGKATLTDSSTAYMHLSSLTSSEDSAVYFCARSS 120
QY 121 DAFDI---WGQGTMTVSSASTKGPSVFPL 147
Db 121 YSYDLFAYWGQGTITVSSAAKTTTPSVYPL 150

RESULT 15
Q99L25 ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181006O009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9898B7986DA155 CRC64;

Query Match 54.8%; Score 431.5; DB 11; Length 473;
Best Local Similarity 52.6%; Pred. No. 5.8e-32;
Matches 81; Conservative 24; Mismatches 42; Indels 7; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKPGASVKVSKVSGYTLTLPVHWVQAP 60
Db 1 MEWSWVFLFELSVTTGVSQVQLQSDAELVKPGASVKVSKVSGYFTDTHHWKQRP 60
QY 61 KGLEWVGSFDPESGESIYAREFOGVSVMYADTSTDIAYMELSLRSDDTAVYCAVPDP 120
Db 61 GQGLEWIGIYIPRDGSKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGS 120
QY 121 -----DAFDIWGQGTMTVSSASTKGPSVFPL 147
Db 121 IYGVGLYFYFDYWGQGTITVSSAKTTAPSVYPL 154

Search completed: April 5, 2004, 13:42:03
Job time : 34.9797 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:09:21 ; Search time 48.4772 Seconds
(without alignments)
874.270 Million cell updates/sec

Title: US-10-044-569B-2

Perfect score: 788
Sequence: 1 MDWTWRILFLVAAATGTHAQ.....MTVSSASTKGPSVFPLGSR 150

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788	100.0	150	4	AAB47058 Heavy cha
2	788	100.0	150	5	AAO18876 Human B02
3	645.5	81.9	535	4	AAAM1145 Human pol
4	627.5	79.6	146	2	AAV24372 Human mon
5	625.5	79.4	146	2	AAV24371 Human mon
6	617	78.3	528	4	AAW39359 Human pol
7	590	74.9	470	5	AAU74236 Anti-huma
8	580.5	73.7	471	7	ADE28427 Human ant
9	563.5	71.5	467	4	AAB36210 Human imm
10	545.5	69.2	219	3	AAV96302 Human IGF
11	539	68.4	476	2	AAW8464 Morocloa
12	536	68.0	652	2	AAW48650 Heavy cha
13	535.5	68.0	249	2	AAV77610 Humanised
14	535	67.9	117	2	AAV66316 Human imm
15	532	67.5	476	6	ABU08022 Morocloa
16	526.5	66.8	249	2	AAV77615 Humanised
17	525	66.6	120	4	AAW39164 Human pol
18	525	66.6	470	3	AAW90935 Humanised
19	525	66.6	470	3	AAW90933 Humanised
20	525	66.6	470	5	ABV74904 Mouse hum
21	525	66.6	470	5	ABV74902 Humanised
22	524	66.5	470	3	AAW90934 Humanised
23	524	66.5	470	5	ABV74903 Mouse hum
24	523	66.4	470	3	AAW90936 Humanised
25	523	66.4	470	5	ABV74945 Humanised

26	522.5	66.3	236	4	AAB36215	Aab36215 Human imm
27	522	66.2	470	2	AAW83037	Aaw83037 Anti-Pas
28	522	66.2	470	3	ABV14779	Abv14779 Humanised
29	522	66.2	470	3	AAW90929	Aaw90929 Humanised
30	522	66.2	470	5	ABV74944	Abv74944 Humanised
31	522	66.2	470	5	ABV74898	Abv74898 Humanised
32	521.5	66.2	197	5	ABP43131	Abp43131 Human Ova
33	519.5	65.9	481	2	AAV24442	Aar24442 Sequence
34	518.5	65.8	515	4	AAW52162	Aam52162 Humanised
35	518.5	65.8	517	4	AAW52154	Aam52154 Humanised
36	518.5	65.8	519	4	AAW52165	Aam52165 Humanised
37	518.5	65.8	519	4	AAW52164	Aam52164 Humanised
38	518.5	65.8	521	4	AAW52163	Aam52163 Humanised
39	518.5	65.8	525	4	AAW52166	Aam52166 Humanised
40	518.5	65.8	527	4	AAW52155	Aam52155 Humanised
41	518.5	65.8	529	4	AAW52168	Aam52168 Humanised
42	518.5	65.8	531	4	AAW52167	Aam52167 Humanised
43	518.5	65.8	729	4	AAW52158	Aam52158 Humanised
44	518.5	65.8	730	4	AAW52157	Aam52157 Humanised
45	518.5	65.8	731	4	AAW52156	Aam52156 Humanised

ALIGNMENTS

RESULT 1

AAB47058
ID AAB47058 standard; protein; 150 AA.

XX AAB47058;

XX AC (first entry)

XX DT 08-MAY-2001

XX DE Heavy chain variable region VH of B02C11.

XX KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;
KW complementarity determining region; CDR; WAB; B02C11;
KW conformational epitope; factor VIII; KR1X1; von Willebrand factor;
KW hemostasis; intravascular coagulation; arterial thrombosis;
KW arterial restenosis; venous thrombosis; arteriosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 44..53

FT Domain /label= CDR1

FT Domain 68..86

FT Domain /label= CDR2

FT Domain 115..125

FT Domain /label= CDR3

XX WO200104269-A1.

XX PD 18-JAN-2001.

XX PF 13-JUL-2000; 2000WO-EP006677.

XX PR 14-JUL-1999; 99GB-00016450.

XX PR 14-JUL-1999; 99US-0143891P.

XX PA (LEUV-) LEUVEN RES & DEV VZW.

XX PI Jacquemin MG, Saint-Remy JR;

XX DR WPI; 2001-138333/14.

XX DR N-PSDB; AAC85451.

XX PT Novel cell lines for producing monoclonal antibodies that bind to a

XX PT factor involved in hemostasis and coagulation cascade, useful for

XX PT treating and preventing coagulation disorders.

XX PS Example 5; Fig 6; 55pp; English.

CC This sequence represents the heavy chain variable region of the human
 CC monoclonal antibody (MAB), B02C11. B02C11 is a human MAB which recognises
 CC a conformational epitope within the carboxy-terminal of the factor VIII
 CC light chain. B02C11 recognises both the wild type and Arg2150His factor
 CC VIII light chains. The MAB produced by the cell line of the invention,
 CC KR1X1, specifically recognises the wild type factor VIII light chain.
 CC KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand
 CC factor in a dose dependant manner. The new cell line KR1X1, is deposited
 CC with the Belgian Coordinated Collections of Micro-organisms, under
 CC accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with
 CC a thrombolytic agent, are useful for the treatment and/or prevention of
 CC haemostasis, coagulation disorder or thrombotic pathologic condition such
 CC as intravascular coagulation, arterial thrombosis, arterial restenosis,
 CC venous thrombosis or arteriosclerosis, and attenuation of coagulation in
 CC a mammal. An effective and safe antithrombotic therapy is provided which
 CC reduces the risk of bleeding in mammals, more particularly in humans
 XX

XX Sequence 150 AA;

Query Match 100.0%; Score 788; DB 4; Length 150;
 Best Local Similarity 100.0%; Pred. No. 8.1e-61;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
 DB 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
 QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 DB 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 QY 121 DAFDINGQGTMTVSSASTKGPSVFPLGSR 150
 DB 121 DAFDINGQGTMTVSSASTKGPSVFPLGSR 150

RESULT 2

AAO18876
 ID AAO18876 standard; protein; 150 AA.

AC AAO18876;

DT 07-NOV-2002 (first entry)

XX Human B02C11 heavy chain variable region.

XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
 KW complementarity determining region; antibacterial; antiinflammatory.

XX Homo sapiens.

Key Location/Qualifiers
 FT Region 44..53
 FT /label= CDR1
 FT Region 68..86
 FT /label= CDR2
 FT Region 115..125
 FT /label= CDR3

XX EPI222929-A2.

XX 17-JUL-2002.

XX 11-JAN-2002; 2002EP-00447005.

XX 11-JAN-2001; 2001US-0261405P.

XX (COLL-) COLLEN RES FOUND VZW D.

XX Jacquemin MG, Saint-Remy JR;

XX

XX WPI; 2002-610270/66.
 DR N-PSDB; AAL49254.

XX Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 PT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.

XX Disclosure; Fig 10; 41pp; English.

XX The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the heavy chain variable region of B02C11

XX Sequence 150 AA;

Query Match 100.0%; Score 788; DB 5; Length 150;
 Best Local Similarity 100.0%; Pred. No. 8.1e-61;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
 DB 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
 QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 DB 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
 QY 121 DAFDINGQGTMTVSSASTKGPSVFPLGSR 150
 DB 121 DAFDINGQGTMTVSSASTKGPSVFPLGSR 150

RESULT 3

AAO41145

ID AAO41145 standard; protein; 535 AA.

AC AAO41145;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6076.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX

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PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AA160301.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 6076; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA158442-AA162213) with neurotropic,
CC immunosuppressant and cytosstatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 535 AA;
SQ
Query Match 81.9%; Score 645.5; DB 4; Length 535;
Best Local Similarity 84.5%; Pred. No. 8.2e-48;
Matches 125; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
QY 1 MDWTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVQAP 60
DB 15 MDCTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVQAP 74
QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 120
DB 75 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCATDHG 134
QY 121 D-AFDIWGQGTMTVSSASTKGPSVFPL 147
DB 135 DYAPDIWGQGTMTVSSASTKGPSVFPL 162
RESULT 4
AA124372
ID AAY24372 standard; protein; 146 AA.
XX
XX AAY24372;
AC
XX
XX 17-SEP-1999 (first entry)
DT
XX
XX Human monoclonal antibody against CTGF SEQ ID NO:12.
DE
XX
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
KW cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
KW skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
KW rheumatic vascular inflammation.
XX
XX Homo sapiens.
OS
XX
XX WO9933878-A1.
PN
XX
XX 08-JUL-1999.
PD
XX
XX 16-DEC-1998; 98WO-JP005697.
PF
XX
XX 25-DEC-1997; 97JP-00367699.
PR
XX
XX 15-DEC-1998; 98JP-00356183.
PR
XX
XX (NIBS) JAPAN TOBACCO INC.
PA
XX
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
PI
XX
XX WPI: 1999-430232/36.
DR N-PSDB; AAX90022.
DR

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PR 15-DEC-1998; 98JP-00356183.
XX
XX (NIBS) JAPAN TOBACCO INC.
XX
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
PI
XX
XX WPI: 1999-430232/36.
DR N-PSDB; AAX90023.
XX
XX New monoclonal antibody reactive with connective tissue growth factor
PT useful in the treatment of cell proliferation disorders.
XX
XX Claim 17; Page 184-185; 212pp; Japanese.
XX
XX AAX90020 to AAX90029 encode monoclonal antibodies which react with human
CC connective tissue growth factor (CTGF). AAX24369 to AAX24378 represent
CC these monoclonal antibodies. The antibodies are useful in the diagnosis,
CC prevention and treatment of cell proliferation disorders in which CTGF is
CC implicated, including fibrosis of lung, kidney, liver and other tissues;
CC liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis;
CC rheumatic vascular inflammation; hepatitis; and cancer
XX
XX Sequence 146 AA;
SQ
Query Match 79.6%; Score 627.5; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 7.1e-47;
Matches 123; Conservative 7; Mismatches 13; Indels 3; Gaps 1;
QY 1 MDWTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVQAP 60
DB 1 MDCTWRIFLVAAATGTHAQVQVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCAVPDP 117
DB 61 GKGLWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYCATSTV 120
QY 118 PDPAPDIWGQGTMTVSSASTKGPS 143
DB 121 VTPWFYDYGQGTMTVSSASTKGPS 146
RESULT 5
AA124371
ID AAY24371 standard; protein; 146 AA.
XX
XX AAY24371;
AC
XX
XX 17-SEP-1999 (first entry)
DT
XX
XX Human monoclonal antibody against CTGF SEQ ID NO:10.
DE
XX
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
KW cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
KW skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
KW rheumatic vascular inflammation.
XX
XX Homo sapiens.
OS
XX
XX WO9933878-A1.
PN
XX
XX 08-JUL-1999.
PD
XX
XX 16-DEC-1998; 98WO-JP005697.
PF
XX
XX 25-DEC-1997; 97JP-00367699.
PR
XX
XX 15-DEC-1998; 98JP-00356183.
PR
XX
XX (NIBS) JAPAN TOBACCO INC.
PA
XX
XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
PI
XX
XX WPI: 1999-430232/36.
DR N-PSDB; AAX90022.
DR

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PR 18-MAY-2000; 2000JP-00147116.
PR 30-MAR-2001; 2001JP-00099508.
XX
PA (NIBS ) JAPAN TOBACCO INC.
XX
PI Tsuji T, Tezuka K, Hori N;
XX
PI WPI; 2002-075313/10.
DR N-PSDB; AAS99472.
XX
XX New human monoclonal antibody that binds to activation inducible
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT arthritis, multiple sclerosis and inflammation.
XX
XX Claim 30; Page 264-266; 300pp; English.
XX
XX The invention relates to a novel human antibody (I), preferably a human
CC monoclonal antibody which binds to an activation inducible lymphocyte
CC immunomodulatory molecule (AIIIM). (I) is useful for modulating signal
CC transduction into a cell mediated by AIIIM, for modulating proliferation
CC of AIIIM-expressing cells, for modulating production of a cytokine from
CC AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC against AIIIM-expressing cells and/or immune cytotoxicity or apoptosis of
CC AIIIM-expressing cells. (I) is useful for treating, preventing or
CC prophylaxis of delayed type allergy. (I) is useful for treating and
CC preventing various diseases associated with AIIIM-mediated costimulatory
CC transduction, and for inhibiting the onset and/or advancement of the
CC diseases. (I) is useful for suppression, prevention and/or treatment of
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC host reaction, graft versus host disease, immune rejection, disorders
CC caused by abnormal intestinal immunity, specifically inflammatory
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC immunorejection due to antigenicity to human, i.e., human anti-mouse
CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
CC AIIIM monoclonal antibody amino acid sequences of the invention
XX
XX Sequence 470 AA;
Query Match 74.9%; Score 590; DB 5; Length 470;
Best Local Similarity 75.5%; Pred. No. 4.7e-43;
Matches 11; Conservative 8; Mismatches 22; Indels 8; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPVMHWGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPVMHWGQAP 60
QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYVCAPV 118
Db 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYVCAPV 118
QY 61 GQGLEWGWINPHSGGTNYAQKFGQVTRDTSISTAYMELSLRSDDTAVYVCARTY 120
Db 61 GQGLEWGWINPHSGGTNYAQKFGQVTRDTSISTAYMELSLRSDDTAVYVCARTY 120
QY 119 -----DPDAFDIWGGQTMVTSSASTKGPSVFPPL 147
Db 121 YDSSGYHDAFDIWGGQTMVTSSASTKGPSVFPPL 155
RESULT 8
ADE28427
ID ADE28427 standard; protein; 471 AA.
XX
AC ADE28427;
XX
DT 29-JAN-2004 (first entry)
XX
XX Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX human; variable region heavy chain; 21-2-1.
XX
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XX Homo sapiens.
XX WO2003040170-A2.
XX 15-MAY-2003.
XX 08-NOV-2002; 2002WO-US036107.
XX 09-NOV-2001; 2001US-0348980P.
XX (PFIZ ) PFIZER PROD INC.
XX (ABGE-) ABGENIX INC.
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX WPI; 2003-441521/41.
XX N-PSDB; ADE28426.
XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
XX Claim 1; SEQ ID NO 34; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region heavy chain protein of the invention.
XX
XX Sequence 471 AA;
Query Match 73.7%; Score 580.5; DB 7; Length 471;
Best Local Similarity 72.4%; Pred. No. 3.2e-42;
Matches 113; Conservative 11; Mismatches 23; Indels 9; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPVMHWGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVLVQSGAEVKKPGASVKVSCKVSGYTLTSLPVMHWGQAP 60
QY 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYVCAPDP 120
Db 61 GKLEWVGSFDPESGESIYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYVCAPDP 120
QY 121 -----DAFDIWGGQTMVTSSASTKGPSVFPPL 147
Db 121 LGYCTNGVCSYFDYWGQTLVTVSSASTKGPSVFPPL 156
RESULT 9
AAB36210
ID AAB36210 standard; protein; 467 AA.
XX
AC AAB36210;
XX
DT 15-FEB-2001 (first entry)
XX
XX Human immune system associated protein HISAP-8.
XX Human; immune system associated protein; HISAP-8; immune disorder;
XX infection; autoimmune disease; cancer.
XX
XX Homo sapiens.
XX US6135941-A.
XX
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XX PD 24-OCT-2000.
XX PF 27-MAR-1998; 98US-00049672.
XX PR 27-MAR-1998; 98US-00049672.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
XX PI Hillman JL, Au-Yang J;
XX DR WPI; 2001-030926/04.
XX DR N-PSDB; AAC66526.
XX PT New human immune system associated proteins (HISAP) and polynucleotides
XX FT encoding the HISAP, useful for diagnosing, treating or preventing immune
XX FT or cell proliferative disorders or infections.
XX PS Claim 1; Col 61-64; 54pp; English.
XX PS Claim 1; Col 61-64; 54pp; English.
XX CC The present invention provides the coding and protein sequences for a
XX CC number of human immune system associated proteins (HISAPs). These can be
XX CC used in the diagnosis and treatment of various autoimmune disorders,
XX CC infections and cell proliferation diseases. The diseases include AIDS,
XX CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
XX CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
XX CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
XX CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX SQ Sequence 467 AA;
Query Match 71.5%; Score 563.5; DB 4; Length 467;
Best Local Similarity 73.0%; Pred. No. 9.5e-41;
Matches 108; Conservative 19; Mismatches 20; Indels 1; Gaps 1;
QY 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
DB 1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFGSVTMDTDTDIAYMELSLRSDDTAVYCAVDP 120
DB 61 GQGLEWNGGLAPENGEAVYAKFLGRITLSDTSAUTAYMFLNLGSEDAIYYCARQHY 120
QY 121 D-AFDINGQGTMTVTVSSASTKGPSVFPL 147
DB 121 DFFDFEWGQGTMTVTVSSASTKGPSVFPL 148
RESULT 10
AAI96302
ID AAY96302 standard; protein; 219 AA.
AC AAY96302;
DT 16-AUG-2000 (first entry)
XX Human IGFAM-14 immunoglobulin.
XX Human; immunoglobulin; IGFAM-14; IGFAM; immune disorder; cancer;
XX infection; inflammation; haematopoiesis; AIDS; allergy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..119
XX Protein 20..219 /label= signal_peptide
XX Domain 34..117 /label= IGFAM-14
XX /label= Ig_domain
XX WO200029583-A2.

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XX PD 25-MAY-2000.
XX PF 19-NOV-1999; 99WO-US027566.
XX PR 19-NOV-1998; 98US-00195853.
XX PR 22-DEC-1998; 98US-0113635P.
XX PR 07-APR-1999; 99US-0128194P.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX PI Lu DAM, Lal P, Hillman JL, Yang J;
XX DR WPI; 2000-387796/33.
XX DR N-PSDB; AAA27394.
XX PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX FT protein is useful for preventing and treating disorders associated with
XX FT altered levels of the protein such as cancer, immune system disorders.
XX PS Claim 1; Page 88-89; 105pp; English.
XX CC The present sequence is the human immunoglobulin superfamily protein
XX CC IGFAM-14. Its gene was isolated from a cDNA library of gallbladder
XX CC tissue. It is expressed in reproductive, gastrointestinal and
XX CC cardiovascular tissue, where cancer and inflammation are common. The
XX CC gene, protein, its antibodies, agonists and antagonists are suitable for
XX CC diagnosing and treating many diseases, including cancer, immune system
XX CC disorders (such as inflammation, AIDS, allergies, anaemia,
XX CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX CC systemic lupus erythematosus and ulcerative colitis), complications of
XX CC cancer, haemodialysis and extracorporeal circulation, trauma and
XX CC haematopoietic cancer (such as leukaemia) and infections caused by
XX CC bacteria, viruses, fungi or parasites
XX SQ Sequence 219 AA;
Query Match 69.2%; Score 545.5; DB 3; Length 219;
Best Local Similarity 69.7%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 5; Gaps 1;
QY 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
DB 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFGSVTMDTDTDIAYMELSLRSDDTAVYCAVCA--- 116
DB 61 GQGLEWNGWNIINPNSGGARYAQGFGLVTMTDTTSISTAYLELRGLRSDGSNAVFCAQTT 120
QY 117 -VPDPAFDINGQGTMTVTVSSASTKGPSVFPL 147
DB 121 SSPVGDAFDINGQGTMTVTVSSASTKGPSVFPL 152
RESULT 11
AAW88464
ID AAW88464 standard; protein; 476 AA.
XX AC AAW88464;
XX DT 10-MAY-1999 (first entry)
XX DE Monoclonal antibody 4B5 heavy chain variable region.
XX Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
XX diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
XX lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
XX Homo sapiens.
XX

```

PN WO9902545-A2.
 XX 21-JAN-1999.
 XX 08-JUL-1998; 98WO-IB001046.
 XX 08-JUL-1997; 97US-0051945P.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX Dan MD;
 XX WPI; 1999-120769/10.
 DR N-PSDB; AAX06951.
 XX New antibody 4B5 polynucleotides and polypeptides - used to develop
 PT products for the diagnosis and treatment of cancers and for prophylactic
 PT therapy to reduce risk of recurrence.
 XX
 XX Claim 1; Page 79-80; 83pp: English.
 XX This polypeptide comprises the heavy chain variable region of the
 CC recombinant human monoclonal antibody (Mab) 4B5. 4B5 recognises
 CC antibodies specific for GD2 antigen antibodies. Antibodies specific for
 CC GD2 recognise various cancers including glioblastoma, neuroblastoma,
 CC malignant and/or metastatic melanoma, breast adenocarcinoma, lung
 CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
 CC immunologic specificity for antibodies specific for GD2. These
 CC derivatives, or antigen binding fragments, comprise regions of the 4B5
 CC VDJ function and regions spanning the 4B5 CDRs. Other derivatives include
 CC Fab, Fab', Fab', scFv and isolated heavy and light chains (see also
 CC AAW8465). Polynucleotide fragments (see AAX06951-54) encoding 4B5
 CC antibody V regions are also provided, and therapeutic plasmids and
 CC vectors, including vaccinia virus vectors, comprising these
 CC polynucleotides. 4B5 has been shown to mimic GD2, and is particularly
 CC useful in generating a host immune response to cancer. Products of the
 CC invention can be used in the detection and treatment of e.g. astrocytoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, primitive neural
 CC ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
 CC large cell lung adenocarcinomas, squamous cell carcinoma,
 CC bronchoalveolar carcinoma, epithelial adenocarcinoma, and liver metastases,
 CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
 CC adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
 CC uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
 CC transitional squamous cell carcinoma of the bladder, B and T cell
 CC lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
 CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma
 XX
 SQ Sequence 476 AA;
 Query Match 68.4%; Score 539; DB 2; Length 476;
 Best Local Similarity 66.9%; Pred. No. 1.3e-38;
 Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;
 QY 1 MDWTRILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
 DB 1 MDWTRVFLVAATSAARSQVQLVQSGAEVKKPGASVKVSGYTLTLPVHWGQAP 60
 QY 61 GKGLWVGSFDPGSGESIIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYVC----- 115
 DB 61 GQGLEWNGWNPNSGKTGYAQKFGRTVTRNTSIRTAYMELSLRSDDTAVYFCARNAD 120
 QY 116 -----AVPDPDAFDWGQGTMTVTVSSASTKGPSVFPL 147
 DB 121 NVENAAIHYHYGMDVWGQGTITVTVSSASTKGPSVFPL 157
 RESULT 12
 ID AAW48650
 XX AAW48650 standard; protein; 652 AA.
 AC AAW48650;

XX 04-AUG-1998 (first entry)
 XX Heavy chain of hmb425 fused to TNF alpha.
 DE Antibody-cytokine fusion protein; tritronic vector; chimeric;
 XX TNF alpha; IL-2; IRES; internal ribosome entry site.
 KW Synthetic.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 XX Region 1.494
 FT /note= "Heavy chain of human mAb 425"
 FT Region 495..652
 FT /note= "TNF alpha"
 FT
 XX WO9811241-A1.
 PN 19-MAR-1998.
 XX 02-SEP-1997; 97WO-EP004765.
 XX 16-SEP-1996; 96EP-00114820.
 PR 30-SEP-1996; 96EP-00115635.
 XX (MERE) MERCK PATENT GMBH.
 XX Von Hoegen I, Burge C, Bruemmer W, Dunker R, Rieke E, Weige T;
 PI Hauser H, Mielke C;
 XX WPI; 1998-207400/18.
 DR N-PSDB; AAV18096.
 XX Oligocistronic expression vector - useful for production of, e.g.
 PT MAb425/TNF- α or MAb425/IL-2 antibody fusion protein.
 PT Disclosure; Fig 15; 89pp; English.
 XX The present sequence represents a fusion protein comprising of TNF alpha
 CC fused to the C-terminus of the heavy chain of the human monoclonal
 CC antibody 425 (hmb425). The hmb425 has specificity for the human EGF
 CC receptor. The invention claims for a new pMCDHAP tritronic vector
 CC (AAV18096) for the expression of an antibody-cytokine fusion protein,
 CC hmb425-TNF alpha. The TNF alpha sequence can be substituted by the IL-2
 CC sequence. The vector also contains a strong promoter/enhancer unit, a
 CC selection marker gene and at least two poliovirus derived internal
 CC ribosomal entry site (IRES) sequences. The vector can be expressed in
 CC mammalian host cells for the production of heteromeric fusion proteins.
 CC This expression system is claimed to produce the heteromeric proteins in
 CC high yields
 XX
 SQ Sequence 652 AA;
 Query Match 68.0%; Score 536; DB 2; Length 652;
 Best Local Similarity 60.6%; Pred. No. 3.4e-38;
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 DB 61 GQGLEWIGEFNPNNGRTNYNEKPKSKATMTVDTSTNTAYMELSLRSDDTAVYVCASRDY 120
 QY 121 D-----AFDIWGQGTMTVTVSS-----ASTKGPSVFPL 147
 DB 121 DYDGRYFDYWGQGTITVTVSSGENILCAWAQLCTPFRSHGTTSLAASKGPSVFPL 175
 RESULT 13
 AAR77610

AAR77610 standard; protein; 249 AA.
 AAR77610;
 25-MAR-2003 (revised)
 15-MAR-1996 (first entry)
 Humanised 5G1.1 VH + IGHL.
 Complement C5; haemolysis; kidney; glomerulonephritis;
 monoclonal antibody; antiinflammatory; antibody engineering;
 humanised antibody; complementarity determining region; CDR.
 Synthetic.
 Key Location/Qualifiers
 Peptide 1..19
 /label= sig_peptide
 Peptide 20..249
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 Region 45..54
 /label= CDR-H1
 Region 69..79
 /label= CDR-H2
 Region 118..130
 /label= CDR-H3
 WO9529697-A1.
 09-NOV-1995.
 01-MAY-1995; 95WO-US0005688.
 02-MAY-1994; 94US-00236208.
 (ALEX-) ALEXION PHARM INC.
 Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
 Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;
 WPI; 1995-392923/50.
 N-PSDB; AAT08483.
 Treating glomerulonephritis with antibody against complement C5 component
 - to inhibit complement induced cell lysis.
 Example 11; Page 119-122; 181pp; English.
 A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH +
 IGHL (AAR77610), includes CDRs derived from mouse anti-C5 monoclonal
 antibody 5G1.1. It can be co-expressed with a humanised light chain
 (AAR77612) in human 293 EBNA cells using encoding DNAs subcloned into
 vector APEX-3P (AAR08476). Such humanised recombinant antibodies retain
 the ability of Mab 5G1.1 to block human complement C5a generation and
 thus to reduce glomerular inflammation and kidney dysfunction associated
 with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)
 Query Match 68.0%; Score 535.5; DB 2; Length 249;
 Best Local Similarity 69.1%; Pred. No. 1.3e-38;
 Matches 105; Conservative 15; Mismatches 27; Indels 5; Gaps 2;
 QY 1 MDWTWILLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYITLTPVHWGQAP 60
 Db 1 MKNSWVILFLSVAAGHVSQVQLVQSGAEVKKPGASVKVSCKASGYIFSNWIQWRQAP 60
 QY 61 GKGLEWVGSDPESGESIVAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCA--- 116
 Db 61 GQGLEWVGILPESGSGSTEVAQFQGRVTMTADTSTDIAYMELSLRSDDTAVYCARFFF 120
 QY 117 VPDPP-AFDINGGNTVTVSSASTKGPSVFPL 147

AAR77610 standard; protein; 249 AA.
 AAR77610;
 25-MAR-2003 (revised)
 15-MAR-1996 (first entry)
 Humanised 5G1.1 VH + IGHL.
 Complement C5; haemolysis; kidney; glomerulonephritis;
 monoclonal antibody; antiinflammatory; antibody engineering;
 humanised antibody; complementarity determining region; CDR.
 Synthetic.
 Key Location/Qualifiers
 Peptide 1..19
 /label= sig_peptide
 Peptide 20..249
 /label= mat_peptide
 Region 45..54
 /label= CDR-H1
 Region 69..79
 /label= CDR-H2
 Region 118..130
 /label= CDR-H3
 WO9529697-A1.
 09-NOV-1995.
 01-MAY-1995; 95WO-US0005688.
 02-MAY-1994; 94US-00236208.
 (ALEX-) ALEXION PHARM INC.
 Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
 Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;
 WPI; 1995-392923/50.
 N-PSDB; AAT08483.
 Treating glomerulonephritis with antibody against complement C5 component
 - to inhibit complement induced cell lysis.
 Example 11; Page 119-122; 181pp; English.
 A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH +
 IGHL (AAR77610), includes CDRs derived from mouse anti-C5 monoclonal
 antibody 5G1.1. It can be co-expressed with a humanised light chain
 (AAR77612) in human 293 EBNA cells using encoding DNAs subcloned into
 vector APEX-3P (AAR08476). Such humanised recombinant antibodies retain
 the ability of Mab 5G1.1 to block human complement C5a generation and
 thus to reduce glomerular inflammation and kidney dysfunction associated
 with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)
 Query Match 68.0%; Score 535.5; DB 2; Length 249;
 Best Local Similarity 69.1%; Pred. No. 1.3e-38;
 Matches 105; Conservative 15; Mismatches 27; Indels 5; Gaps 2;
 QY 1 MDWTWILLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYITLTPVHWGQAP 60
 DB 1 MKNSWVILFLSVAAGHVSQVQLVQSGAEVKKPGASVKVSCKASGYIFSNWIQWRQAP 60
 QY 61 GKGLEWVGSDPESGESIVAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCA--- 116
 DB 61 GQGLEWVGILPESGSGSTEAQKFGQGVMTADTSTDIAYMELSLRSDDTAVYCARFFF 120
 QY 117 VPDPP-AFDINGGCTVMTVSSASTKGPSVFPL 147

XX AC ABU08022;
 XX DT 10-MAY-2003 (first entry)
 XX DE Monoclonal rabies virus antibody heavy chain, clone 57.
 XX KW Human; antibody; constant region; monoclonal antibody 57; Mab 57;
 XX KW variable region; Rabies; neurological disease; infection;
 XX KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
 XX KW pathogen; vaccine; virucide; heavy chain.
 XX OS Homo sapiens.
 XX PN WO2003016501-A2.
 XX PD 27-FEB-2003.
 XX PF 21-AUG-2002; 2002WO-US026584.
 XX PR 21-AUG-2001; 2001US-0314023P.
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX PI Hooper DC, Dietzschold B;
 XX DR WPI; 2003-278566/27.
 XX DR N-PSDB; ABX12864.
 XX PT New recombinant antibody comprising a constant region of Mab 57 linked to
 PT a non-Mab 57 variable region, useful for treating an individual exposed
 PT to a pathogen, e.g. rabies infection.
 XX PS Claim 1; Page 38; 38pp; English.
 XX CC The invention discloses a recombinant antibody comprising a constant
 CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
 CC region. Rabies is an acute, neurological disease caused by infection of
 CC the central nervous system with the rabies virus, a member of the
 CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
 CC for producing an isolated recombinant antibody by culturing a host cell,
 CC containing a recombinant expression vector comprising the nucleic acid
 CC molecule encoding the antibody, and isolating the recombinant antibody
 CC expressed and treating an individual exposed to a pathogen by
 CC administering to the individual the recombinant antibody. The recombinant
 CC antibodies are useful for preventing (vaccine) and treating an individual
 CC exposed to a pathogen, e.g. rabies infection. They are also useful for
 CC the qualitative and quantitative determination of the rabies virus. The
 CC sequences presented are the antibody protein fragments, the nucleic acids
 CC encoding them or the PCR primers used to construct the recombinant
 CC expression vector
 XX SQ Sequence 476 AA;
 Query Match 67.5%; Score 532; DB 6; Length 476;
 Best Local Similarity 67.5%; Pred. No. 5.3e-38;
 Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;
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 DB 61 GKGLEWVGSFDPESGESIYAREFGQSVMTADTSTDIAYMELSSLSRSDDTAVYYCAVPDP 120
 QY 121 DA-----FDIWGGTMTVSSASTKGPSVPEL 147
 DB 121 DNSGTYYFSGWFDPWGQGLTVTVSSASTKGPSVPEL 157

Search completed: April 5, 2004, 13:24:15
 Job time : 50.4772 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 35.2792 Seconds
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Perfect score: 788
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
Maximum Match 100%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	788	100.0	150	14	US-10-044-569B-2
2	627.5	79.6	146	14	US-10-390-986-12
3	625.5	79.4	146	14	US-10-390-986-10
4	590	74.9	470	9	US-09-859-053-28
5	539	68.4	476	9	US-09-747-669-3
6	539	68.4	476	14	US-10-290-703-3
7	532	67.5	476	14	US-10-225-108A-16
8	532	67.5	476	15	US-10-461-148-9
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11	525	66.6	470	14	US-10-384-933-143
12	525	66.6	470	14	US-10-384-933-147
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					Sequence 157, Appl

16	523	66.4	470	14	US-10-384-933-157
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18	522	66.2	470	14	US-10-384-933-117
19	521.5	66.2	197	15	US-10-264-049-4263
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23	518.5	65.8	519	9	US-09-825-012-80
24	518.5	65.8	521	9	US-09-825-012-71
25	518.5	65.8	525	9	US-09-825-012-85
26	518.5	65.8	527	9	US-09-825-012-43
27	518.5	65.8	529	9	US-09-825-012-95
28	518.5	65.8	531	9	US-09-825-012-90
29	518.5	65.8	729	9	US-09-825-012-52
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34	518.5	65.8	741	9	US-09-825-012-55
35	516	65.5	574	13	US-10-047-542-45
36	516	65.5	574	14	US-10-214-524-37
37	516	65.5	574	14	US-10-050-902-176
38	516	65.5	574	14	US-10-050-898-176
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ALIGNMENTS

RESULT 1

US-10-044-569B-2
; Sequence 2, Application US/10044569B
; Publication No. US20030175269A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (130)..(159)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202)..(258)
; OTHER INFORMATION: complementary determining region number two
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; NAME/KEY: misc feature
; LOCATION: (343)..(375)
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; OTHER INFORMATION: complementary determining region number three

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Best Local Similarity 100.0%; Pred. No. 4, 5e-63;
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Db 61 GKGLWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 120
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RESULT 2
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; Sequence 12, Application US/10390986
; Publication No. US2003016601A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
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; ORGANISM: Homo sapiens
US-10-390-986-12

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; Sequence 10, Application US/10390986
; Publication No. US2003016601A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
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US-10-390-986-10

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QY 61 GKGLWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCAVDP 118
Db 61 GKGLWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSLRSDDTAVYCATSV 120

RESULT 4
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
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; ORGANISM: Homo sapiens
US-09-859-053-28

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RESULT 5
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; Patent No. US20020122807A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
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; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Synthetic construct
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Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;

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DB 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARNAD 120
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157

; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

Query Match      67.5%; Score 532; DB 14; Length 476;
Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
DB 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
QY 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARENL 120
DB 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARENL 120
QY 121 DA-----FDINGQGTMTVSSASTKGPSVFPL 147
DB 121 DNSGTYFFSGWFDPMGQGTITVSSASTKGPSVFPL 157

; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

RESULT 6
US-10-290-703-3
; Sequence 3, Application US/10290703
; Publication No. US20030118933A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-703-3

Query Match      68.4%; Score 539; DB 14; Length 476;
Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60

```

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; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-3

Query Match      68.4%; Score 539; DB 9; Length 476;
Best Local Similarity 66.9%; Pred. No. 3.6e-40;
Matches 105; Conservative 16; Mismatches 26; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYC----- 115
DB 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYC----- 115
QY 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARNAD 120
DB 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARNAD 120
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157
QY 116 -----AVPDPDAFDINGQGTMTVSSASTKGPSVFPL 147
DB 121 NVEMAALHYHYGMDVWGQGTITVSSASTKGPSVFPL 157

; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

Query Match      67.5%; Score 532; DB 14; Length 476;
Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
DB 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
QY 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARENL 120
DB 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARENL 120
QY 121 DA-----FDINGQGTMTVSSASTKGPSVFPL 147
DB 121 DNSGTYFFSGWFDPMGQGTITVSSASTKGPSVFPL 157

; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

RESULT 7
US-10-225-108A-16
; Sequence 16, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCES: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

Query Match      67.5%; Score 532; DB 14; Length 476;
Best Local Similarity 67.5%; Pred. No. 1.5e-39;
Matches 106; Conservative 13; Mismatches 28; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
DB 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGVTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
DB 61 GKGLWVGSFDPESGSIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
QY 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARENL 120
DB 61 GQGLEWNGWNPNSGKTGYAQKFGQGRVTMTNTSIRTAYMELSLGRSEDTAVYFCARENL 120
QY 121 DA-----FDINGQGTMTVSSASTKGPSVFPL 147
DB 121 DNSGTYFFSGWFDPMGQGTITVSSASTKGPSVFPL 157

; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-16

RESULT 8
US-10-461-148-9
; Sequence 9, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; APPLICANT: Hooper, Douglas C.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04

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Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
DB 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA--- 116
DB 61 GGGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCARNRD 120
QY 117 VPDPADFIDWQGTMTVSSASTKGPSVPEL 147
DB 121 YSNWYFDVWGQTLTVSSASTKGPSVPEL 151

RESULT 12
US-10-384-933-147
; Sequence 147, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-147

Query Match 66.6%; Score 525; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 6.3e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
DB 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA--- 116
DB 61 GGGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCARNRD 120
QY 117 VPDPADFIDWQGTMTVSSASTKGPSVPEL 147
DB 121 YSNWYFDVWGQTLTVSSASTKGPSVPEL 151

RESULT 13
US-10-216-484-145
; Sequence 145, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG

CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 145
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-145

Query Match 66.5%; Score 524; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 7.8e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
DB 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA--- 116
DB 61 GGGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCARNRD 120
QY 117 VPDPADFIDWQGTMTVSSASTKGPSVPEL 147
DB 121 YSNWYFDVWGQTLTVSSASTKGPSVPEL 151

RESULT 14
US-10-384-933-145
; Sequence 145, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 145
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-145

Query Match 66.5%; Score 524; DB 14; Length 470;
Best Local Similarity 68.2%; Pred. No. 7.8e-39;
Matches 103; Conservative 14; Mismatches 30; Indels 4; Gaps 1;
QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
DB 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKVSGYTLTLPVHWVGQAP 60
QY 61 GKGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCA--- 116
DB 61 GGGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCARNRD 120

RESULT 2
US-09-582-337-10
; Sequence 10, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337

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; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-337-10

Query Match      79.4%; Score 625.5; DB 4; Length 146;
Best Local Similarity 84.2%; Pred. No. 6.4e-51;
Matches 123; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYGLTSLPVMHWGOAP 60
DB 1 MDCTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYGLTSLPVMHWGOAP 60
QY 61 GKGLEWVSGFPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCA---V 117
DB 61 GKGLEWVSGFPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCATSTV 120
QY 118 PDPADPIWGQGTWTVSSASTKGPS 143
DB 121 VTPWYFDYWGQGTWTVSSASTKGPS 146

RESULT 3
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Kal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 2747531
; LIBRARY: LUNGITUT11
; ORGANISM: Homo sapiens
US-09-049-672A-8

Query Match      71.5%; Score 563.5; DB 3; Length 467;
Best Local Similarity 73.0%; Pred. No. 1.4e-44;
Matches 108; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MDWTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYGLTSLPVMHWGOAP 60
DB 1 MDCTWRIILFLVAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYGLTSLPVMHWGOAP 60
QY 61 GKGLEWVSGFPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDF 120
DB 61 GCGLEWVSGFPESGESIYAREFGQSVTMTADTSTDIAYMELSLRSDDTAVYYCAVDPDF 120
QY 121 D-AFDWGGTMTVTVSSASTKGPSVFPL 147
DB 121 DFFDFWGGTMTVTVSSASTKGPSVFPL 148

RESULT 4
US-08-545-809A-110
; Sequence 110, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-110

Query Match      67.9%; Score 535; DB 3; Length 117;
Best Local Similarity 87.9%; Pred. No. 1.3e-42;
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Matches 102; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLPWHVWGQAP 60
DB 1 MDCTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAP 60

QY 61 GKGLWVGSGFDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCA 116
DB 61 GKGLWVGSGFDPEDGETIYIAQKPGQVMTEDTSTDIAYMELSSLRSDDTAVYYCA 116

RESULT 5
US-09-049-672A-13
; Sequence 13, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Marian R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNNOT01
; CLONE: 3551457
US-09-049-672A-13

Query Match 66.3%; Score 522.5; DB 3; Length 236;
Best Local Similarity 67.3%; Pred. No. 4e-41;
Matches 101; Conservative 16; Mismatches 30; Indels 3; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLPWHVWGQAP 60
DB 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMHWVRQAP 60

QY 61 GKGLWVGSGFDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCA ---V 117

Db 61 GQLEWNGWLNAGNGTKYSONFGQRTITRDTASATAYMELSSLRSDTAVYYCARVWA 120
QY 118 PDPAFDIMGQGTMTVTYSSASTKGPSVFPL 147
Db 121 GEFTSFYDWGQGLTIVTSSASPTSPKVFRL 150

RESULT 6
US-08-513-968-38
; Sequence 38, Application US/08513968
; Patent No. 6114143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-513-968-38

Query Match 65.2%; Score 513.5; DB 3; Length 137;
Best Local Similarity 69.3%; Pred. No. 1.5e-40;
Matches 95; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

QY 1 MDWTRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVCKVSGYTLTSLPWHVWGQAP 60
DB 1 MDWTRVFCILAVAPGASQVQLVQSGAEVKKPGASVKVCKASGTFTEYTHHWVRQAP 60

QY 61 GKGLWVGSGFDPESGSIYAREFGQSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-D 119
Db 61 GQGLEWIGGINPNNGTSYTKPKGKATMTVDTSINTAYMELSSLRSDTAVYYCATPY 120

QY 120 PDPAFDIMGQGTMTVSS 136
Db 121 AYADISWGQGLTIVTSS 137

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; Sequence 10, Application US/08378939
; Patent No. 5879361
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U. S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-939-10

Query Match 64.0%; Score 504; DB 2; Length 476;
Best Local Similarity 62.5%; Pred. No. 4.7e-39;
Matches 100; Conservative 16; Mismatches 28; Indels 16; Gaps 2;

Qy 1 MDMTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWGQAP 60
Db 1 MDMTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWGQAP 60
Qy 61 GKGLEWVSGFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Db 61 GKGLEWVSGFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Qy 121 DA-----FDIWGGTMTVSSASTKGPSVFPL 147
Db 118 DRYQANFDRARVGVFDPWGQGLTVTVSSASTKGPSVFPL 157

RESULT 9
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29

; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U. S. A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-45

Query Match 65.0%; Score 512.5; DB 2; Length 467;
Best Local Similarity 64.5%; Pred. No. 7.4e-40;
Matches 98; Conservative 17; Mismatches 32; Indels 5; Gaps 1;

Qy 1 MDMTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWGQAP 60
Db 1 MDMTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKYSCKVSGYTLTLPVHWGQAP 60
Qy 61 GKGLEWVSGFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Db 61 GKGLEWVSGFDPESGESIYAREFGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDP 120
Qy 121 DA-----FDIWGGTMTVSSASTKGPSVFPL 147
Db 121 NYATGANFAYWGQGLTVTVSSASTKGPSVFPL 152

RESULT 8
US-08-378-939-10
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; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo.sapiens
US-09-301-593-43

Query Match      63.8%; Score 503; DB 4; Length 472;
Best Local Similarity 63.8%; Pred. No. 5.7e-39;
Matches 98; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

Qy 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVHWVQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MDWTWRFVCLLAVAPGAHSQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVHWVQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 GKGLWVGSFDPESGESIYAREFQGSVTMTADTSTDIAWMELSLRSDDTAVYYCA---- 116
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 GORLEWIGINFNNGIPNTNQKFGKRAITLVGKSASTAYMELSLRSEDTAVYYCARRRI 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 117 ----VPDPDAFDIWGQGTWTVSSASTKGPSVFPL 147
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 AYCDEGHAMDYWGQGTTLTVSS-STKGPSVFPL 153
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
US-07-946-421-28
; Sequence 28, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettlesborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-28

Query Match      63.6%; Score 501; DB 1; Length 140;
Best Local Similarity 68.6%; Pred. No. 2.2e-39;
Matches 96; Conservative 14; Mismatches 26; Indels 4; Gaps 1;

Qy 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVHWVQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MDWTWRFVCLLAVAPGAHSQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVHWVQAP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 GKGLWVGSFDPESGESIYAREFQGSVTMTADTSTDIAWMELSLRSDDTAVYYCAVPDP 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 GQGLEWVGEPNPNNGRTNNTYNEKFSRVMTLDTSTAYMELSLRSEDTAVYYCASRDY 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 121 D----AFDIWGQGTWTVSS 136
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 DYDGRVFDYWGQGTTLTVSS 140
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
US-09-582-337-8
; Sequence 8, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: JI-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-337-8

Query Match      62.9%; Score 496; DB 4; Length 149;
Best Local Similarity 66.9%; Pred. No. 6.9e-39;
Matches 103; Conservative 9; Mismatches 26; Indels 16; Gaps 3;

Qy 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVH 54
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MDWTWRLFLVAAATGTHAQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVH 55
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 55 WVGQAPGKGLWVGSFDPESGESIYAREFQGSVTMTADTSTDIAWMELSLRSDDTAVYY 114
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 56 WVRQAPGQGLEWVGWINPNSSGTHYAQMFGQVTRVTRDTSISTAYMELSLRSDDTAVYY 115
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 115 CAVDPDPA-----FDIWGQGTWTVSSASTKGPS 143
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 116 CAREGIAAAIYGMVWGQGTTLTVSSASTKGPS 149
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 12
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
```

NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 62.5%; Score 492.5; DB 1; Length 135;
Best Local Similarity 68.4%; Pred. No. 1.3e-38;
Matches 93; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
Qy 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYSTSYIHWVRQAP 60
Qy 61 GKGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
Db 61 GQGLEWIGYIDPFNGGTSYNOKFKGKVTMTVDTSTNTAYMELSLRSEDATVYYCA-RGG 119
Qy 121 DAFDWGGTMTVYSS 136
Db 120 NRFAWGGTILTVSS 135

RESULT 13
US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-102

Query Match 62.5%; Score 492.5; DB 2; Length 135;
Best Local Similarity 68.4%; Pred. No. 1.3e-38;
Matches 93; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
Qy 1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYSTSYIHWVRQAP 60
Qy 61 GKGLWVGSFDPESGESIYAREFOGVTMTADTSTDIAYMELSLRSDDTAVYYCAVPDP 120
Db 61 GQGLEWIGYIDPFNGGTSYNOKFKGKVTMTVDTSTNTAYMELSLRSEDATVYYCA-RGG 119
Qy 121 DAFDWGGTMTVYSS 136
Db 120 NRFAWGGTILTVSS 135

RESULT 14
US-08-649-100-41
Sequence 41, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-PAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-PAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-649-100-41

Query Match 62.4%; Score 492; DB 3; Length 136;
Best Local Similarity 68.4%; Pred. No. 1.5e-38;
Matches 93; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Qy 61 GKLEWVGSPDPGSGESYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYICAVPDP 120
Db 61 GKLEWVGSPDPGSGESYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYICAVPDP 120
Qy 121 DAFDINGQGTMTVTSS 136
Db 121 DYFDYWGQGLTVTVSS 136

RESULT 15

US-08-137-117D-100
Sequence 100, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-100

Query Match 62.0%; Score 488.5; DB 1; Length 135;
Best Local Similarity 68.4%; Pred. No. 3.1e-38;
Matches 93; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Db 1 MDWTRILFLVAAATGTHAQVQVQSGAEVKKPGASVKVSCKVSGYTLTLPVHWGQAP 60
Qy 61 GKLEWVGSPDPGSGESYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYICAVPDP 120
Db 61 GKLEWVGSPDPGSGESYAREFGSVTMTADTSTDIAYMELSLRSDDTAVYICAVPDP 120
Qy 121 DAFDINGQGTMTVTSS 136
Db 121 NRFAWGGGLTVTVSS 135

Search completed: April 5, 2004, 13:44:08
Job time: 14.4518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 11.533 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 METPAQLLFLLMLPDTTG.....TRLEIKGTVAAPSVFIIPPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	85.9	129	S49532	anti-Sm antibody V
2	627	85.5	145	S20631	Ig kappa chain - h
3	624	85.1	129	K3H0HA	Ig kappa chain pre
4	614	83.8	129	K3H0HI	Ig kappa chain pre
5	614	83.8	129	S46369	Ig light chain var
6	614	83.8	134	S38643	Ig kappa chain v r
7	608.5	83.0	144	PL0106	Ig kappa chain pre
8	608	82.9	128	S20636	Ig kappa chain v r
9	596	81.3	121	S40327	Ig kappa chain - h
10	594	81.0	130	S20637	Ig kappa chain v r
11	591	80.6	129	A32274	Ig kappa chain pre
12	576	78.6	124	S20633	Ig kappa chain - h
13	574	78.3	116	B27594	Ig kappa chain pre
14	567.5	77.4	131	S40346	Ig kappa chain V-J
15	563.5	76.9	126	S40325	Ig kappa chain - h
16	560.5	76.5	116	C227594	Ig kappa chain pre
17	557.5	76.1	128	K3H041	Ig kappa chain pre
18	553	75.4	130	S40360	Ig kappa chain - h
19	549	74.9	127	S40380	Ig kappa chain V-J
20	547	74.6	116	B22521	Ig kappa chain pre
21	540.5	73.7	128	S40343	Ig kappa chain V-J
22	537	73.3	129	S40363	Ig kappa chain - h
23	534.5	72.9	128	S40379	Ig kappa chain V-J
24	533	72.7	215	JE0242	Ig kappa chain NIG
25	532.5	72.6	114	S46375	Ig kappa chain V-J
26	531.5	72.5	128	A56701	Ig kappa chain v r
27	530	72.3	215	A23746	Ig kappa chain V-I
28	522.5	71.3	129	S29627	Ig kappa chain v r
29	520	70.9	109	B30601	Ig kappa chain V-I

30 520 70.9 109 2 H30601 Ig kappa chain V-I
31 519.5 70.9 125 2 S40344 Ig kappa chain V-J
32 518 70.7 108 2 C30608 Ig kappa chain V-I
33 517 70.5 109 2 C30601 Ig kappa chain V-I
34 515 70.3 109 2 D30601 Ig kappa chain V-I
35 513 70.0 109 2 G30601 Ig kappa chain V-I
36 513 70.0 116 2 S41917 Ig kappa chain V-I
37 510 69.6 109 2 PH0963 Ig kappa chain V-I
38 510 69.6 109 2 F30607 Ig kappa chain V-I
39 510 69.6 109 2 F30601 Ig kappa chain V-I
40 508.5 69.4 115 1 K3HUVG Ig kappa chain pre
41 508 69.3 107 2 PH0965 Ig kappa chain V-J
42 508 69.3 111 2 S40359 Ig kappa chain V-J
43 508 69.3 118 2 T03036 Ig light chain - h
44 506.5 69.1 128 2 S40345 Ig kappa chain V-J
45 506 69.0 116 1 K3HUVH Ig kappa chain pre

ALIGNMENTS

RESULT 1

S49532
anti-Sm antibody VL chain (V kappa 3/5 kappa 2) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49532
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
A:Submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <MAH>
A:Cross-references: EMBL:Z46345; NID:G560843; PIDN:CAA86464.1; PID:G560844
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMW>

Query Match 85.9%; Score 630; DB 2; Length 129;

Best Local Similarity 94.5%; Pred. No. 4.7e-43;
Matches 121; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 METPAQLLFLLMLPDTTGTEIATQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
Db 1 METPAQLLFLLMLPDTTGTEIATQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
Qy 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYTCOKYGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYTCOKYGTSAITFG 120
Qy 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 2

S20631
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20631
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
A:Submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20631
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <LEE>
A:Cross-references: EMBL:Z11903; NID:G33156; PIDN:CAA77955.1; PID:G33157
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMW>


```
Query Match      85.5%; Score 627; DB 1; Length 145;
Best Local Similarity 83.8%; Pred. No. 9e-43;
Matches 119; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128
QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 3
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0022
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      85.1%; Score 624; DB 1; Length 129;
Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 120; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 4
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0021
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      85.1%; Score 624; DB 1; Length 129;
Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 120; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 5
S46369
IG light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46369
R:Benjamin, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46369
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <BEN>
A:Cross-references: EMBL:Z27170
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      83.8%; Score 614; DB 2; Length 129;
Best Local Similarity 92.2%; Pred. No. 8.5e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
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```
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0021
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      83.8%; Score 614; DB 1; Length 129;
Best Local Similarity 92.2%; Pred. No. 8.5e-42;
Matches 118; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
QY 121 QGTRLEIK 128
DB 121 QGTRLEIK 128

RESULT 5
S46369
IG light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46369
R:Benjamin, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46369
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <BEN>
A:Cross-references: EMBL:Z27170
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      83.8%; Score 614; DB 2; Length 129;
Best Local Similarity 92.2%; Pred. No. 8.5e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
DB 1 METPAQLLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCOYKGTSAITFG 120
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```
QY 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 6
S38643
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
R:Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A:Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A:Reference number: S38643
A:Accession: S38643
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <BEN>
A:Cross-references: EMBL:Z27170; NID:G415955; PIDN:CAA81694.1; PID:G415956
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-116/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 614; DB 2; Length 134;
Best Local Similarity 92.2%; Pred. No. 8.8e-42; Mismatches 6; Indels 0; Gaps 0;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
Db 6 METPAQVLFLLLLWLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 65

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
Db 66 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPFPFG 125

QY 121 QGTRLEIK 128
Db 126 QGTRLEIK 133

RESULT 7
P10106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: P10106; MUID:89235583; PMID:2541221
A:Accession: P10106
A:Molecule type: mRNA
A:Residues: 1-144 <SL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 83.08%; Score 608.5; DB 2; Length 144;
Best Local Similarity 85.2%; Pred. No. 2.6e-41;
Matches 121; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 METPAQLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
Db 1 MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOR 59

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
Db 60 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQORSNWLPTFG 119

QY 121 QGTRLEIKTVAAAPSVFIPPPS 142
Db 120 GGTKEIKRTVAAAPSVFIPPPS 141

RESULT 8
S20636
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20636
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20636
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <LEE>
A:Cross-references: EMBL:Z11894; NID:G33200; PIDN:CAA77948.1; PID:G33201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 608; DB 2; Length 128;
Best Local Similarity 91.4%; Pred. No. 2.5e-41;
Matches 117; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 METPAQLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
Db 1 METPAQLFLLLLWLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 60

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
Db 61 PQQAPRLIYAASSTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPRPTFG 120

QY 121 QGTRLEIK 128
Db 121 QGTRLEIK 128

RESULT 9
S40327
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40327
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080691; PMID:8258341
A:Accession: S40327
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72437; NID:G441342; PIDN:CAA51105.1; PID:G441343
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-108/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 596; DB 2; Length 121;
Best Local Similarity 94.2%; Pred. No. 2.1e-40;
Matches 114; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 PAQLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOKPGQ 63
Db 1 PAQLFLLLLWLPDTTGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOKPGQ 60

QY 64 APRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 123
```


Db 1 METPAQLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
QY 61 PQCAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYKGTGTS 115
Db 61 PQCAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYKGTGTS 115

RESULT 14
S40346
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40346
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40346
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72456; NID:G441380; PIDN:CAA51124.1; PID:G441381
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-110/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 567.5; DB 2; Length 131;
Best Local Similarity 85.5%; Pred. No. 4e-38;
Matches 112; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
QY 2 ETTPAQLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKP 61
Db 1 ETTPAQLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQHP 60
QY 62 GQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYKGTGTS-AITFG 120
Db 61 GQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCHYKGGSPPTFG 120
QY 121 QGTRLEIKTV 131
Db 121 QGTRLEIKTV 131

RESULT 15
S40325
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40325
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40325
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72435; NID:G441338; PIDN:CAA51103.1; PID:G441339
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-110/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 563.5; DB 2; Length 129;
Best Local Similarity 82.8%; Pred. No. 8.2e-38;
Matches 106; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
QY 2 ETTPAQLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKP 61
Db 1 ETTPAQLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQORP 60
QY 62 GQAPRLIIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYKGTSAI-TFG 120

Db 61 GQAPRLIIYGASTRATGVPDRFSGSGGTDTLTISRMEPEDFAVYCCQYGGSPPLTFG 120
QY 121 QGTRLEIK 128
Db 121 PGTKVDIR 128
Search completed: April 5, 2004, 13:43:02
Job time : 12.533 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:10:21 ; Search time 6.48731 Seconds
(without alignments)
1139.758 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 METPAQLLELLMLPDTTG.....TRLEIKGTVAAPSVFIIPPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	85.1	129	1 KV3L_HUMAN	P18135 homo sapien
2	614	83.8	129	1 KV3M_HUMAN	P18136 homo sapien
3	557.5	76.1	128	1 KV3K_HUMAN	P06311 homo sapien
4	537	73.3	129	1 KV3H_HUMAN	P04207 homo sapien
5	508.5	69.4	115	1 KV3J_HUMAN	P04433 homo sapien
6	506	69.0	116	1 KV3J_HUMAN	P04434 homo sapien
7	505	68.9	109	1 KV3B_HUMAN	P01620 homo sapien
8	502	68.5	109	1 KV3E_HUMAN	P01623 homo sapien
9	498	67.9	109	1 KV3D_HUMAN	P01622 homo sapien
10	489	66.7	108	1 KV3A_HUMAN	P01619 homo sapien
11	482	65.8	109	1 KV3G_HUMAN	P01621 homo sapien
12	466	63.6	100	1 KV3C_HUMAN	P01624 homo sapien
13	447	61.0	109	1 KV3F_HUMAN	P04431 homo sapien
14	427.5	58.3	129	1 KV1W_HUMAN	P04314 homo sapien
15	420.5	57.4	134	1 KV4C_HUMAN	P06313 homo sapien
16	413	56.3	133	1 KV4B_HUMAN	P01602 homo sapien
17	404.5	55.2	117	1 KV1J_HUMAN	P01661 mus musculu
18	399.5	54.5	131	1 KV4J_HUMAN	P01625 homo sapien
19	395.5	54.0	114	1 KV4A_HUMAN	P06310 homo sapien
20	394	53.8	133	1 KV2F_HUMAN	P01658 mus musculu
21	390.5	53.3	132	1 KV3F_HUMAN	P01600 homo sapien
22	381.5	52.0	108	1 KV1H_HUMAN	P01605 homo sapien
23	380.5	51.9	108	1 KV1M_HUMAN	P06312 homo sapien
24	379.5	51.8	121	1 KV4C_HUMAN	P06312 homo sapien
25	379.5	51.8	129	1 KV1X_HUMAN	P04432 homo sapien
26	378.5	51.6	128	1 KV5E_HUMAN	P01637 mus musculu
27	376.5	51.4	108	1 KV1F_HUMAN	P01598 homo sapien
28	376.5	51.4	108	1 KV1Q_HUMAN	P01609 homo sapien
29	370.5	50.5	149	1 KV5A_HUMAN	P01633 mus musculu
30	369.5	50.4	108	1 KV1D_HUMAN	P01596 homo sapien
31	366	49.9	107	1 KV1D_HUMAN	P01604 homo sapien
32	365.5	49.9	108	1 KV1V_HUMAN	P04430 homo sapien
33	365.5	49.9	108	1 KV1V_HUMAN	P04430 homo sapien

RESULT 1

KV3L_HUMAN 113 49.8 365 49.7 113 1 KV2D_HUMAN P01617 homo sapien
KV3L_HUMAN 108 49.7 364.5 49.5 108 1 KV1N_HUMAN P01606 homo sapien
AC P18135, 108 49.5 362.5 48.9 108 1 KV1K_HUMAN P01603 homo sapien
DT 01-NOV-1990 (Rel. 16, Created) 117 48.9 358.5 48.5 117 1 KV1I_HUMAN P01601 homo sapien
DT 01-NOV-1990 (Rel. 16, Last sequence update) 108 48.5 355.5 48.5 108 1 KV1R_HUMAN P01610 homo sapien
DT 15-JUL-1999 (Rel. 38, Last annotation update) 109 48.5 355.5 48.5 109 1 KV4D_HUMAN P83593 homo sapien
DE Ig kappa chain V-III region HAH precursor. 136 48.2 353.5 48.0 136 1 KV5B_MOUSE P01634 mus musculu
OS Homo sapiens (Human). 111 48.0 351.5 48.0 111 1 KV3W_MOUSE P01665 mus musculu
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; 108 47.8 350.5 47.8 108 1 KV1A_HUMAN P01593 homo sapien
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 111 47.7 350.5 47.7 111 1 KV3N_MOUSE P01666 mus musculu
OX NCBI_TaxID=9606; 108 47.7 349.5 47.7 108 1 KV1E_HUMAN P01597 homo sapien
RN [1] 117 47.6 349 47.6 117 1 KV2E_HUMAN P06309 homo sapien

ALIGNMENTS

SEQUENCE FROM N.A.
MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tonhave E., Chen P.P., Carson D.A.;
"Antibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988)
-I- DISEASE: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.

PIR; PLO022; K3HUHA.
HSP; P80362; LWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_Like; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 UKI SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C552927774D0 CRC64;

Query Match 85.1%; Score 624; DB 1; Length 129;
Best Local Similarity 93.8%; Pred. No. 1.3e-53;
Matches 129; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 METPAQLLELLMLPDTTGGEATLTSPGTLSCRAQSSSSSYLAWYQOK 60
Db 1 METPAQLLELLMLPDTTGGEATLTSPGTLSCRAQSSSSSYLAWYQOK 60
Qy 61 PGQAPRLLIYGASTRATGIPDRFSGSGSGCTDFTLTISRLEPEDFAVYVYQKYGTSAITFG 120

Db	61	PCQAPRLIIVYGASSRATGIPDRFGSGSGDFTLTISRLPEPFVAVYCCQYGTSPRTFG	120
Qy	121	QGTRLEIK 128	
Db	121	QGTRKEIK 128	
 RESULT 2 KV3M_HUMAN			
ID	KV3M_HUMAN	STANDARD; PRT; 129 AA.	
AC	Pt8136;		
DT	01-NOV-1990 (Rel. 16, Created)		
DT	01-NOV-1990 (Rel. 16, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-III region HIC precursor.		
DE	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBTaxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=88171307; PubMed=3127527;		
RA	Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;		
RT	"Autoantibody-associated kappa light chain variable region gene		
RT	expressed in chronic lymphocytic leukemia with little or no somatic		
RT	mutation. Implications for etiology and immunotherapy.";		
RL	J. Exp Med. 167:840-852(1988).		
CC	-!- DISASE: the protein is one of the surface immunoglobulin M		
CC	autoantibodies expressed in patients with chronic lymphocytic		
CC	leukemia.		
PIR	PLC021; K3HUHI.		
DR	HSSP; P80362; IWL.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003596; IG_V.		
DR	Ffam; PF00047; Ig/I.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
DR	Immunoglobulin V region; Signal.		
FT	SIGNAL 1 20		
FT	CHAIN 21 129	IG KAPPA CHAIN V-III REGION HIC.	
FT	DOMAIN 21 43	FRAMEWORK-1.	
FT	DOMAIN 44 55	CPLEMENTARITY-DETERMINING-1.	
FT	DOMAIN 56 70	FRAMEWORK-2.	
FT	DOMAIN 71 77	CPLEMENTARITY-DETERMINING-2.	
FT	DOMAIN 78 109	FRAMEWORK-3.	
FT	DOMAIN 110 118	CPLEMENTARITY-DETERMINING-3.	
FT	DOMAIN 119 129	JK1 SEGMENT.	
FT	DISULFID 43 109	BY SIMILARITY.	
FT	NON_TER 129 129		
SEQ	SEQUENCE 129 AA; 14070 MW; 7395528EA2B874D6 CRC64;		
 Query Match 83.8%; Score 614; DB 1; Length 129; Best Local Similarity 92.2%; Pred. No. 1.2e-52; Matches 118; Conservative 5; Mismatches 5; Indels 0; Gaps 0			
Qy	1	METPAQLFLLLMLLPDTTGBIALTQSPGTLSPGERATLSCRASQSFSSSYLAHYQQK 60	
Db	1	METPAQLFLLLMLLPDTTGBIVLTQSPGTLSPGERATLSCRASQSVSSSYLAHYQQK 60	
Qy	61	PCQAPRLIIVYGASTATGIPDRFGSGSGDFTLTISRLPEPFVAVYCCQYGTSAITFG 120	
Db	61	PCQAPRLIIVYGASSRATGIPDRFGSGSGDFTLTISRLPEPFVAVYCCQYGTSAITFG 120	
Qy	121	QGTRLEIK 128	
Db	121	QGTRKEIK 128	

RESULT 3

4

```

KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC F06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region IARC/BL41 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobock H.G., Meindl A., Conbratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC or send an email to license@isb-sib.ch).
EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR HSP; P01607; LRE1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0005955; P:immune response; NAS.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DISULFID
FT DISULFID
FT NON_TER
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match
Best Local Similarity 76.1%; Score 557.5; DB 1; Length 128;
Matches 11; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 1 METPAQLLELLILWLPDITGEIALTQSPGTLSPGERATLSCRASQSSESSYLAWYQQK 60
DB 1 METPAQLLELLILWLPDITGEIVLTQSPGTLSLPGESATLSCRASQSVSN-LAWYQQK 59

QY 61 PQGAPELLLYGASTRATG;PDRFGSGSGCTDFTLTISRLEPEDFAVYYCKYGTSAITFG 120
DB 60 RQSPALLLRDASSRANGIPDRFGSGSGCTDFTLISRLEPEDFAVYYCQQTSTSYTFG 119

QY 121 QQTRLEIK 128
DB 120 QGTKLEIK 127

```

RESULT 4

KV3H_HUMAN
ID_KV3H_HUMAN
AC P04207;

Query Match	76.1%;	Score 557.5;	DB 1;	Length 128;
Best Local Similarity	86.7%;	Pred. No. 3.6e-47;		
Matches 11:	Conservative	5;	Mismatches 11;	Indels 1;
				Gaps 1;

Qy 1 METPAQLFLLLIWL PDTTGEIALTQSPGTLSLSPGERATISCRASQSFSSSYLAWYQOK 60

Db 1 METPAQLFLLLIWL PDTTGEIALTQSPGTLSLSPGERATISCRASQSVSSN:LAWYQOK 59

Qy 61 PGQAPRLLYGASTRATGIPDRPGSGSGTDFTLTISRLEPEDFAVYVCQKYSATTFG 12

Qy	121	QGTRLEIK	128
		:	
pb	120	QGTKEIK	127

KV3H_HUMAN	STANDARD;	PRT;	129 AA.
ID_KV3H_HUMAN			
AC_P04207			

DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region C-III precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177570; PubMed=2083417;
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M12740; AAA58992.1; --
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20 IG KAPPA CHAIN V-III REGION CELL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 119 129 JK1 SEGMENT.
 FT NON_TER 43 108 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
 Query Match 73.3%; Score 537; DB 1; Length 129;
 Best Local Similarity 82.9%; Pred. No. 3.6e-45;
 Matches 107; Conservative 8; Mismatches 12; Indels 2; Gaps 2;
 QY 1 METPAQLFLLLMLPDTTGTGIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
 DB 1 MEAPAQFLFLLLMLPDTTGTGIVNTQSPATLSVSPGERATLSGRASQSVNN-LAWYQOK 59
 QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTFTLTISRLEPEDFAVYCYCKGT-SALTIF 119
 DB 60 PQQAPRLIYGASTRATGIPARFSGSGGTFTLTISRLOSEDFAVYCYCQNNWPPWTF 119
 QY 120 GQTRLEIK 128
 DB 120 GQTRVEIK 128
 RESULT 5
 KV3J_HUMAN STANDARD; PRT; 115 AA.
 ID KV3J_HUMAN
 AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus".
 RL Nucleic Acids Res. 12:9229-9236(1984).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X01568; --; NOT_ANNOTATED_CDS.
 DR PIR; A01900; K3HUVG.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 >115 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
 Query Match 69.4%; Score 508.5; DB 1; Length 115;
 Best Local Similarity 91.0%; Pred. No. 1.8e-42;
 Matches 101; Conservative 1; Mismatches 8; Indels 1; Gaps 1;
 QY 1 METPAQLFLLLMLPDTTGTGIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
 DB 1 MEAPAQFLFLLLMLPDTTGTGIVNTQSPATLSVSPGERATLSGRASQSV-SSYLAWYQOK 59
 QY 61 PQQAPRLIYGASTRATGIPDRFSGSGGTFTLTISRLEPEDFAVYCYCK 111
 DB 60 PQQAPRLIYGASTRATGIPARFSGSGGTFTLTISRLEPEDFAVYCYCQ 110
 RESULT 6
 KV3J_HUMAN STANDARD; PRT; 116 AA.
 ID KV3J_HUMAN
 AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VH precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;

Pech M., Zachau H.G.;
 "Immunoglobulin genes of different subgroups are interdigitated
 within the VK locus";
 Nucleic Acids Res. 12:9229-9236(1984).

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 or send an email to license@isb-sib.ch).

 EMBL; X02725; -; NOT_ANNOTATED_CDS.
 PIR; A01901; K3HUVH.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12757 MW; 51CD55BAS3B21929 CRC64;
 Query Match 69.0%; Score 506; DB 1; Length 116;
 Best Local Similarity 88.3%; Pred. No. 3.2e-42;
 Matches 98; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 QY 1 METPAQLFLLLNLWIPDTTGIALTQSPGTLSPGERATLSCRASQSFSSYLAWYQOK 60
 DB 1 MEAPAQFLFLLLNLWIPDTTRELVTQSPGTLSPGERATLSCRASQSVSSYLWYQOK 60
 QY 61 PQCAPRLTYGASTRATGIPRFGSGSGTDTFTLTISRLEPEDFAVYCYQK 111
 DB 61 PQCAPRLTYGASTRATGIPRFGSGSGTDTFTLTISRLEPEDFAVYCYQK 111
 RESULT 7
 KV3B_HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human Igm anti-gamma-globulins of the wa
 RT group";
 RL Biochemistry 20:5816-5822(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01892; K3HUVL.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;
 Query Match 68.5%; Score 502; DB 1; Length 109;
 Best Local Similarity 88.9%; Pred. No. 7.2e-42;
 Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSYLAWYQOKPQAPRLTYGASTRATGIP 80
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLWYQOKPQAPRLTYGASTRATGIP 60
 QY 81 DRFGSGSGTDTFTLTISRLEPEDFAVYCYQKTSAITFGQTRLEIK 128
 DB 81 DRFGSGSGTDTFTLTISRLEPEDFAVYCYQKTSAITFGQTRLEIK 108

HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3EC6D46FFB4 CRC64;
 Query Match 68.9%; Score 505; DB 1; Length 109;
 Best Local Similarity 88.9%; Pred. No. 3.7e-42;
 Matches 96; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSYLAWYQOKPQAPRLTYGASTRATGIP 80
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLWYQOKPQAPRLTYGASTRATGIP 60
 QY 81 DRFGSGSGTDTFTLTISRLEPEDFAVYCYQKTSAITFGQTRLEIK 128
 DB 61 DRFGSGSGTDTFTLTISRLEPEDFAVYCYQKTSAITFGQSGKVEIK 108
 RESULT 8
 KV3B_HUMAN STANDARD; PRT; 109 AA.
 ID KV3B_HUMAN
 AC P01623;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region WOL.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human Igm anti-gamma-globulins of the wa
 RT group";
 RL Biochemistry 20:5816-5822(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01896; K3HUVL.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;
 Query Match 68.5%; Score 502; DB 1; Length 109;
 Best Local Similarity 88.9%; Pred. No. 7.2e-42;
 Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSYLAWYQOKPQAPRLTYGASTRATGIP 80
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLWYQOKPQAPRLTYGASTRATGIP 60
 QY 81 DRFGSGSGTDTFTLTISRLEPEDFAVYCYQKTSAITFGQTRLEIK 128

DB 61 DRFSGSGGDTFTLTISRLEPEDFAVYCCQYGLRFTGGTKVELK 108
 RESULT 9
 KV3D HUMAN
 ID KV3D HUMAN STANDARD; PRT; 109 AA.
 AC P01622;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region T1.
 DE Ig kappa chain V-III region T1.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72188439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 RT T1). IV. The complete amino acid sequence and its significance for
 RT the mechanism of antibody production.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01895; K3HUT.
 DR HSP; P80362; LWL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89
 FT NON TER 109 109
 FT BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
 Query Match 67.9%; Score 498; DB 1; Length 109;
 Best Local Similarity 88.0%; Pred.No.1.7e-41;
 Matches 95; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 QY 21 EIALTQSPGTLSPGGERATLSCRSASQSFSSYLAWYQKPGQAPRLIIYGASTRATGIP 80
 DB 1 EIVLTQSPGTLSPGGERATLSCRSASQSVNSFLAWYQKPGQAPRLIIYVASSRATGIP 60
 QY 81 DRFSGSGGDTFTLTISRLEPEDFAVYCCQYGTSAITFGGTRLEIK 128
 DB 61 DRFSGSGGDTFTLTISRLEPEDFAVYCCQYGGSPSTFGGTRKVELK 108
 RESULT 10
 KV3A HUMAN
 ID KV3A HUMAN STANDARD; PRT; 108 AA.
 AC P01619;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region B6.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RA Milstein C.;
 RT "The basic sequences of immunoglobulin kappa chains: sequence studies
 RT of Bence Jones proteins Rad, Fr4 and B6.";
 RL FEBS Lett. 2:301-304(1969).

```
RESULT 12
KV3C HUMAN          STANDARD;          PRT;   100 AA.
ID   KV3C HUMAN
AC   P01621;
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region NG9 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093600; PubMed=6419127;
RA   Bentley D.L.;
RT   "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RL   Nature 307:77-80(1984).
CC   -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR   PIR; A01894; K3HUNG.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00406; IGV; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS0835; IG LIKE; 1.
KW   Immunoglobulin V region.
FT   DISULFID 27 93
FT   NON TER 100 100
SQ   SEQUENCE 100 AA; 10729 MW; 5D9AF363C52632F CRC64;
Query Match      63.6%; Score 466; DB 1; Length 100;
Best Local Similarity 91.8%; Pred. No. 2e-38;
Matches 89; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  19 TGETALQSPQTLSLSPGERATLSCRASQSFSSSYLAWYQKQPGQAPRLIIYGASTRATG 78
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  3 SGEIVLQSPQTLSLSPGERATLSCRASQSFSSSYLAWYQKQPGQAPRLIIYGASTRATG 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  79 IPDRFSGSGGTDTLTISRLEPEDFAVYCYQKYGTS 115
Db  63 IPDRFSGSASGTDFTLTISRLEPEDFAVYCYQYQNS 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
KV3F HUMAN          STANDARD;          PRT;   109 AA.
ID   KV3F HUMAN
AC   P01624;
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig kappa chain V-III region POM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76276460; PubMed=60899;
RA   Klapper D.G., Capra J.D.;
RT   "The amino acid sequence of the variable regions of the light chains
RT   from two idiotypically cross reactive IgM anti-gamma globulins.";
RL   Ann. Immunol. (Paris) 127C:261-271(1976).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC   GLOBULIN ACTIVITY.
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DR   PIR; A01897; K3HUPM.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS0835; IG LIKE; 1.
KW   Immunoglobulin V region.
FT   DISULFID 23 89
FT   NON TER 109 109
SQ   SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
Query Match      61.0%; Score 447; DB 1; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.5e-36;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY  21 EIALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQKQPGQAPRLIIYGASTRATGIP 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 EIVMTQSPVTLSPGERATLSCRASQSFSSSYLAWYQKQPGSPRLIIYGASTRATGIP 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  81 DRFGSGSGGTDTLTISRLEPEDFAVYCYQKYGTSALTFGGTRLEIK 128
Db  61 ARFGSGSGGTDTLTISRLEPEDFAVYCYQYNNWPTFGGTRVEIK 108
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
KV1W HUMAN          STANDARD;          PRT;   129 AA.
ID   KV1W HUMAN
AC   P04431.
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobbeck H.G., Combratio G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
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CC   -----
CC   EMBL; X00965; CAA25477.1; ALT_TERM.
CC   PIR; A01883; K1HUMK.
CC   HSSP; P01607; 1REI.
CC   GO; GO:0005576; C:extracellular; NAS.
CC   GO; GO:0003823; F:antigen binding; NAS.
CC   GO; GO:0006955; P:immune response; NAS.
CC   InterPro; IPR007110; Ig-like.
CC   InterPro; IPR003596; Ig_v.
CC   Pfam; PF00047; Ig; 1.
CC   SMART; SM00406; IGV; 1.
CC   PROSITE; PS0835; IG LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL 1 22
FT   CHAIN 23 129
FT   DOMAIN 23 45
FT   DOMAIN 46 56
FT   DOMAIN 57 71
```

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FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 58.3%; Score 427.5; DB 1; Length 129;
Best Local Similarity 56.4%; Pred.No.1.4e-34;
Matches 85; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIATQSPGTLSPGGERATLSGRASQSFSSSYLA 60
DQ 3 MRVPAQLLGLLLWLWLRGARDIQMTQSPSLASVGRVTITCRASQSI-SNYLWYQOK 61
QY 61 PGQAPRLLYGASTRATGIPDRFSGSGGTDFLTITSLRLEPEDFAVYCYOKYGTSAITFG 120
DQ 62 PGKAPKLLLYAASSLQSGVTSRFSGSGGTDFLTITSLRLEPEDFAVYCYOKYGTSAITFG 121
QY 121 QGTRLEIK 128
DQ 122 QGTRLEIK 129

RESULT 15
KV4C HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RA Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; X02990; CAA26733.1; -
CC HSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 20 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 134 FRAMEWORK-1.
FT DOMAIN 21 43 FRAMEWORK-2.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
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FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 57.4%; Score 420.5; DB 1; Length 134;
Best Local Similarity 60.9%; Pred.No.7.1e-34;
Matches 81; Conservative 20; Mismatches 27; Indels 5; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIATQSPGTLSPGGERATLSGRASQSFSSSYLA 55
DQ 1 MVLQTQVFISLLWLWISGAYGDIWVTQSPDLSLGERATINCKSSQSIYSSDNKNYLA 60
QY 56 WYQOKPGCAPLLIYAGSTRATGIPDRFSGSGGTDFLTITSLRLEPEDFAVYCYOKYGTSAITFG 115
DQ 61 WYQOKPGCAPLLIYAGSTRATGIPDRFSGSGGTDFLTITSLRLEPEDFAVYCYOKYGTSAITFG 120
QY 116 AITFGQGTLEIK 128
DQ 121 PWTEGQGTKEIK 133

Search completed: April 5, 2004, 13:24:55
Job time : 6.48731 secs
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:24:21 ; Search time 30.2741 Seconds
(without alignments)
1479.931 Million cell updates/sec

Title: US-10-044-569B-4

Perfect score: 733

Sequence: 1 METPAQLFLLLWLPDTTG.....TRLEIKGTVAPEVFIFPPS 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	68.9	109	4 Q9UL78	Q9UL78 homo sapien
2	495.5	67.6	234	4 Q72473	Q72473 homo sapien
3	491	67.0	109	4 Q9UL46	Q9UL46 homo sapien
4	473.5	64.6	236	4 Q72374	Q72374 homo sapien
5	466	63.6	239	4 Q8NEKO	Q8NEKO homo sapien
6	450	61.4	239	4 Q8TCDO	Q8TCDO homo sapien
7	425.5	58.0	237	13 Q7SZ36	Q7SZ36 xenopus lae
8	424.5	57.9	108	4 Q9UL83	Q9UL83 homo sapien
9	422	57.6	109	4 Q9UL85	Q9UL85 homo sapien
10	413.5	56.4	236	11 Q7TWK3	Q7TWK3 mus musculus
11	413.5	56.4	238	11 Q99M37	Q99M37 mus musculus
12	412.5	56.3	236	11 Q7TS98	Q7TS98 mus musculus
13	406.5	55.5	238	11 Q8VC16	Q8VC16 mus musculus
14	405.5	55.3	234	11 Q8VCP0	Q8VCP0 mus musculus
15	390	53.2	239	11 Q8VC55	Q8VC55 mus musculus
16	389.5	53.1	234	11 Q8R062	Q8R062 mus musculus

17	385	52.5	239	11 Q8KOF8	Q8KOF8 mus musculus
18	382.5	52.2	108	4 Q9UL70	Q9UL70 homo sapien
19	382.5	52.2	234	11 Q9LWF8	Q9LWF8 mus musculus
20	381.5	52.0	108	4 Q9UL79	Q9UL79 homo sapien
21	380.5	51.9	108	4 Q9UL77	Q9UL77 homo sapien
22	377	51.4	107	4 Q9ESA9	Q9ESA9 homo sapien
23	370.5	50.5	131	11 Q811C3	Q811C3 mus musculus
24	366.5	50.0	214	11 Q9RIA5	Q9RIA5 mus musculus
25	364	49.7	114	11 Q8K1F1	Q8K1F1 mus musculus
26	362	49.4	107	4 Q9UL81	Q9UL81 homo sapien
27	360.5	49.2	116	4 Q9EPF6	Q9EPF6 homo sapien
28	360.5	49.2	233	11 Q9LWS9	Q9LWS9 mus musculus
29	360	49.1	235	11 Q9LW12	Q9LW12 mus musculus
30	359	49.0	235	11 Q7TMK0	Q7TMK0 mus musculus
31	345	47.1	112	11 Q8K1F2	Q8K1F2 mus musculus
32	342.5	46.7	298	11 Q9QVFO	Q9QVFO mus musculus
33	342	46.7	112	11 Q8K1F3	Q8K1F3 mus musculus
34	341.5	46.6	111	11 Q92OE9	Q92OE9 mus musculus
35	338.5	46.2	107	11 Q9ERZ3	Q9ERZ3 mus musculus
36	335.5	45.8	148	11 Q8K122	Q8K122 mus musculus
37	334	45.6	106	5 Q9U410	Q9U410 schistosoma
38	333.5	45.5	127	11 Q925S9	Q925S9 mus musculus
39	332	45.3	134	11 Q8VDD0	Q8VDD0 mus musculus
40	330.5	45.1	109	11 Q92OE6	Q92OE6 mus musculus
41	330.5	45.1	234	11 Q8R028	Q8R028 mus musculus
42	328.5	44.8	111	11 Q811U6	Q811U6 mus musculus
43	321.5	43.9	99	11 Q9JL74	Q9JL74 mus musculus
44	320.5	43.7	108	11 Q8VIJ0	Q8VIJ0 mus musculus
45	319	43.5	243	11 Q7TQM2	Q7TQM2 mus musculus

ALIGNMENTS

RESULT 1

Q9UL78	ID	Q9UL78	PRELIMINARY;	PRT;	109 AA.
AC	Q9UL78;				
DT	01-MAY-2000	(TRENBLrel. 13, Created)			
DT	01-MAY-2000	(TRENBLrel. 13, Last sequence update)			
DT	01-OCT-2003	(TRENBLrel. 25, Last annotation update)			
DE	Myosin-reactive immunoglobulin light chain variable region				
DE	(Fragment)				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98277139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RT	fetus."				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035036; AAD56272.1; -				
DR	PIR; A30601; A30601.				
DR	PIR; A30608; A30608.				
DR	PIR; B30601; B30601.				
DR	PIR; B30607; B30607.				
DR	PIR; C30601; C30601.				
DR	PIR; C30607; C30607.				
DR	PIR; C30608; C30608.				
DR	PIR; D30601; D30601.				
DR	PIR; D30607; D30607.				
DR	PIR; D30608; D30608.				
DR	PIR; F30607; F30607.				
DR	PIR; F30608; F30608.				
DR	PIR; G30601; G30601.				
DR	PIR; G30608; G30608.				
DR	PIR; H30607; H30607.				
DR	PIR; H30608; H30608.				
DR	PIR; I30601; I30601.				

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DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 68.9%; Score 505; DB 4; Length 109;
Best Local Similarity 89.8%; Pred. No. 1.1e-44;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDCAVYCYQYGSPLTFGGTKVEIK 108

RESULT 2
Q72473 PRELIMINARY; PRT; 234 AA.
ID Q72473
AC Q72473
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA Krywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C295BAB51BC0F CRC64;

Query Match 67.6%; Score 495.5; DB 4; Length 234;
Best Local Similarity 69.0%; Pred. No. 3e-43;
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Matches 98; Conservative 14; Mismatches 29; Indels 1; Gaps 1;
QY 1 METPAQLLFLLLMLPDTTGTGIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQK 60
Db 1 MRVPAQLLGLLLMLPGARCAIRMTQSPSPSASTGDRVTITCRASQSI-GSYLAWYQK 59

QY 61 PQQAPRLIYGASTRATGIPDRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFG 120
Db 60 PKAPQLLIYAASLTQSQVPRFSGSASGTDTLISLCLOSEDFATYCCQYTYPTWTFG 119

QY 121 QCTRLKIGTVAAPSVFIFFPS 142
Db 120 QGTKEIKRTVAAPSVFIFFPS 141

RESULT 3
Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
AC Q9UL86
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 67.0%; Score 491; DB 4; Length 109;
Best Local Similarity 87.0%; Pred. No. 3.2e-43;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60

QY 81 DRFGSGSGTDFTLTISRLEPEDFAVYCKYGTSAITFCGTRLEIK 128
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYGSIFTFGGTKVDIK 108

RESULT 4
Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4
AC Q723Y4
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=3606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN [2]
RC SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC005332; AAH05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBE4ED23084BC6 CRC64;

Query Match 64.6%; Score 473.5; DB 4; Length 236;
Best Local Similarity 65.5%; Pred. No. 5.8e-41;
Matches 93; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

QY 1 METPAQLLFLILLMLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSPSSYLAWYQOK 60
Db 3 MRVLAQLLGLLLLCFFGARCIDIQMTQSPSSLSASVGTVTITCRASQDI-SNYLAWFQOK 61

QY 61 PQQAPRLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCYCKYGTSAITFG 120
Db 62 PGKAPKSLIYGASSLQSGVSKFSGSGSGTDFTLTISRLEPEDFAVYCYCKYKSPYVTFG 121

QY 121 QGTREIKGTVAAPSVFIFFPS 142
Db 122 QGTREIKRTVAAPSVFIFFPS 143

RESULT 5
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC022362; AAH22362.1; -.
KW PIR; S34095; S34095.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 61.4%; Score 450; DB 4; Length 239;
Best Local Similarity 58.9%; Pred. No. 1.6e-38;
Matches 86; Conservative 27; Mismatches 29; Indels 4; Gaps 1;

QY 1 METPAQLLFLILLMLPDTTGEIALTQSPGTLSLSPGERATLSCRASQSPSSYLAWYQOK 56
Db 1 MRVLAQLLGLLLLCFFGARCIDIQMTQSPSSLSASVGTVTITCRASQDI-SNYLAWFQOK 60

QY 57 YQKPGQAPRLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCYCKYGTSA 116
Db 61 FQKPGQAPRLIYKVSNRDGVDPDRFSGSGSGTDFTLTISRLEPEDFAVYCYCKYGTSA 120

QY 117 ITFGQGTREIKGTVAAPSVFIFFPS 142
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Db 121 STFGQGTLEIKRTVAAPSVFIPEPS 146

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RESULT 7
Q7S236 PRELIMINARY; PRT; 237 AA.
AC Q7S236
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054155; AAH54155.1;
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26300 MW; 47B8D0D2639CEB436 CRC64;

Query Match 58.0%; Score 425.5; DB 13; Length 237;
Best Local Similarity 61.2%; Pred. No. 5.6e-36;
Matches 85; Conservative 20; Mismatches 31; Indels 3; Gaps 1;

QY 7 LFLALLLPDPTTGIALTQPGTILSPGERATISCRASQSF--SSSYLAWYQKPGQ 63
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DE 7 LLPILMLMQSGYGVIVTQPDYVSVPGETVLTCKASSVAIGSTIVLHWYQKSGQ 66
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 64 APRLLIYGASTRATGIPRFSGSGGTFTLTISRLEPEDFAVYVCQKYGTSATFGQGT 123
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DE 67 VPKLILYLANTRHTGTPRISGSGGTFTLTISRMEAEADAAVYCCQSRDPLTFKGT 126
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 124 RLEIKGTVAAPSVFIPEPS 142
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DE 127 RVELKRNDAKPAVFIKFS 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 8

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Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1;
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; P550835; IG LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 57.9%; Score 424.5; DB 4; Length 108;
Best Local Similarity 78.7%; Pred. No. 2.5e-36;
Matches 85; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 21 ETALQTQPTILSPGERATISCRASQSFSSSYLAWYQKPGQAPRLIYGASTRATGIP 80
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DE 1 EIVMTQSPATLSVSPGERATISCRASQSVSSN-LAWYQKPGQAPRLIYGASTRATGIP 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 DRFGSGSGGTDFTLTISRLEPEDFAVYVCQKYGTSATFGQGTLEIK 128
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DE 60 ARFGSGSGGTFTLTISRLEPEDFAVYVCQHYNNWPFPGTKVDIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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DR EMBL: AF035029; AAD56265.1; -.
DR PIR: D30609; D30609.
DR HSP: P80362; 1WT.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 57.6%; Score 422; DB 4; Length 109;
Best Local Similarity 77.1%; Pred. No. 4.7e-36;
Matches 84; Conservative 12; Mismatches 11; Indels 2; Gaps 2;

QY 21 EIALTSPGTLSPGERATLSRCASQSPSSSVLAWYQKPGQAPRLIYGASTRATGIP 80
Db 1 EIVTQSPATLSVSPGERATLSRCASQSSSN-LAWYQKPGQAPRLIYGASTRATGIP 59
QY 81 DRFSGSGGDTFTLTISRLEPEPAVYQKYGCT-SAITFGGQTRLEIK 128
Db 60 ARFSGSGGTEFTLTISRLEPEPAVYHCQYNSWPLTFGGGTVKVIK 108

RESULT 10
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002035; AAH02035.1; -.
DR PIR: A31807; A31807.
DR PIR: A32248; A32248.
DR PIR: B32248; B32248.
DR PIR: C32248; C32248.
DR PIR: F32530; F32530.
DR PIR: PH1042; PH1042.
DR PIR: PH1043; PH1043.
DR PIR: PH1044; PH1044.
DR PIR: S07455; S07455.
DR PIR: S16112; S16112.
DR PIR: S24500; S24500.
DR PIR: S24501; S24501.
DR PIR: S24503; S24503.
DR PIR: S24504; S24504.
DR PIR: S24529; S24529.
DR PIR: S24532; S24532.
DR PIR: S24533; S24533.
DR PIR: S24535; S24535.
DR PIR: S24536; S24536.
DR PIR: S24538; S24538.
DR PDB: 1I91; 25-DEC-02.
DR PDB: 1LO2; 31-JUL-02.
DR PDB: 1LO4; 31-JUL-02.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 56.4%; Score 413.5; DB 11; Length 238;
Best Local Similarity 54.8%; Pred. No. 1e-34;
Matches 80; Conservative 28; Mismatches 33; Indels 5; Gaps 2;

QY 1 METPAQLFLLLWLPTTGTGIALTQSPGTLSPGERATLSRCASQSPSSSVLAWYQK 60
Db 3 MRAPAQFGILLWFPQIRCDIKNTQSPSSMYASLGSRVITCKASODI-KSYLSWYQK 61
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEPAVYQKYGCTSAITFG 120
Db 62 PWKSPKTLIYATSLADGVSRFSGSGGQDYSLTISLSLSDDTATYCYCLQHGSPTFG 121
QY 121 QGTRLEIKGTVAAPSVFIFPPS 142
Db 122 SGTKEIKRADAAFTVSIFPPS 143

RESULT 11
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002035; AAH02035.1; -.
DR PIR: A31807; A31807.
DR PIR: A32248; A32248.
DR PIR: B32248; B32248.
DR PIR: C32248; C32248.
DR PIR: F32530; F32530.
DR PIR: PH1042; PH1042.
DR PIR: PH1043; PH1043.
DR PIR: PH1044; PH1044.
DR PIR: S07455; S07455.
DR PIR: S16112; S16112.
DR PIR: S24500; S24500.
DR PIR: S24501; S24501.
DR PIR: S24503; S24503.
DR PIR: S24504; S24504.
DR PIR: S24529; S24529.
DR PIR: S24532; S24532.
DR PIR: S24533; S24533.
DR PIR: S24535; S24535.
DR PIR: S24536; S24536.
DR PIR: S24538; S24538.
DR PDB: 1I91; 25-DEC-02.
DR PDB: 1LO2; 31-JUL-02.
DR PDB: 1LO4; 31-JUL-02.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 56.4%; Score 413.5; DB 11; Length 238;
Best Local Similarity 54.8%; Pred. No. 1e-34;
Matches 80; Conservative 28; Mismatches 33; Indels 5; Gaps 2;

QY 1 METPAQLFLLLWLPTTGTGIALTQSPGTLSPGERATLSRCASQSPSSSVLAWYQK 56
Db 1 MKLPVRL-LVLMFWIPASSDVMVTQTPSLPVLGQASISCRSSQSIHNSNGNTYLEW 59
QY 57 YQKPGQAPRLIYGASTRATGIPDRFSGSGGDTFTLTISRLEPEPAVYQKYGCTSA 116
```


Db 60 YLQKFGQSKLLIYKYVNRSGVDRFSGSGSGTDFTLKISRVEADLGVYCFQGSHPV 119
QY 117 ITFGQGTREIKGTVAAPSVFIFFPS 142
Db 120 YTFSGGKLEIKRADAAPTVSIFPPS 145

RESULT 12

Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=9372513;
RA Tonge D.W., Hennen J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116NS19.9 heavy and light chain
cDNAs and expression of antibody fragments in *Escherichia coli*."
RL year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; -.
SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;

Query Match 56.3%; Score 412.5; DB 11; Length 236;
Best Local Similarity 56.3%; Pred. No. 1.3e-34;
Matches 80; Conservative 22; Mismatches 39; Indels 1; Gaps 1;
QY 1 METPAQLFLLLMLPDTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAWYQOK 60
Db 3 MRTPAQLGILLWFPKMKCDIKMTQSPFMYASLGERVTITCKASQDI-NSYLSWFQOK 61
QY 61 PQQAPRLIYCASTRATGIDPRFSGSGSGTDFTLTISRLEPDEFVAVYCYCKYGTSAITFG 120
Db 62 PKSKPKLIYRANRLVDGVRFSFGSGSGGQDYSLTSSLEYEDMGIIYCLQYDEFRTFG 121
QY 121 QGTREIKGTVAAPSVFIFFPS 142
Db 122 GGTKEIKRADAAPTVSIFPPS 143

RESULT 13

Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.

DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; FL0257; FL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 55.5%; Score 406.5; DB 11; Length 238;
Best Local Similarity 54.1%; Pred. No. 5.3e-34;
Matches 79; Conservative 29; Mismatches 33; Indels 5; Gaps 2;
QY 1 METPAQLFLLLMLPDTTGEIALTQSPGTLSPGERATLSGRASQSFSSSYLAW 56
Db 1 MKLPVRLR-VLMFPIPASSDVMTQTFSLPVLGDCASISCRSSSLVHSGNTYLHW 59
QY 57 YQKPGQAPRLIYCASTRATGIDPRFSGSGSGTDFTLTISRLEPDEFVAVYCYCKYGTSA 116
Db 60 YLQKFGQSKLLIYKYVNRSGVDRFSGSGSGTDFTLKISRVEADLGVYCFQGSHPV 119
QY 117 ITFGQGTREIKGTVAAPSVFIFFPS 142
Db 120 PTFGGGKLEIKRADAAPTVSIFPPS 145

RESULT 14

Q8VCPO PRELIMINARY; PRT; 234 AA.
AC Q8VCPO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR PIR; B47329; B47329.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.

```
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
Query Match 55.3%; Score 405.5; DB 11; Length 234;
Best Local Similarity 57.7%; Pred. No. 6.6e-34;
Matches 82; Conservative 18; Mismatches 41; Indels 1; Gaps 1;

QY 1 METPAQLLELLILWLPDITGTEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
D 1 MSVPTQVLGLLLCLTGARCDLQLTQSPASLSASVGETVITCRASENI-YSYLAWYQOK 59
QY 61 PQCAPRLIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYCKYGTSAITFG 120
D 60 QKSKQLLYVNAKTLADGVPSRFSRSGTQSLKINSLOPEDFGSYCYQHSGIPPTFG 119
QY 121 QGTRLEIKGTVAAPSFIFFPS 142
D 120 SGTKLEIKRAADAAPTVISIFFPS 141

RESULT 15
Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strauberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC021781; AH21781.1; -
DR PIR; A33933; A33933.
DR PDB; 1KCS; 24-JUL-02.
DR GO; GO:0005576; C:extracellular; IEA.
DR CO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF02950; Conotoxin; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 53.2%; Score 390; DB 11; Length 239;
Best Local Similarity 53.4%; Pred. No. 2.7e-32;
Matches 78; Conservative 27; Mismatches 37; Indels 4; Gaps 1;

QY 1 METPAQLLELLILWLPDITGTEIALTQSPGTLSPGERATLSCRASQSFSS---YLAW 56
D 1 MKLPVLLVLLLTSPASSDDVLTQPLSLPVNIGDQASISCKSTKSLNSDGYLDW 60
QY 57 YQKPGQAPRLIYGATRGATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYCKYGTSA 116
D 61 YLQKPGSQPLIYLVNRFSGVDPDRFSGSGGTDFTLTKISRVEADLGVYCFQSNHLP 120
QY 117 ITFGQGRLEIKGTVAAPSFIFFPS 142
D 121 YTFGGTKLEIKRAADAAPTVISIFFPS 146

Search completed: April 5, 2004, 13:42:05
Job time : 32.2741 secs
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CC This sequence represents the light chain variable region of the human
 CC monoclonal antibody (MAB), B02C11. B02C11 is a human MAB which recognises
 CC a conformational epitope within the carboxy-terminal of the factor VIII
 CC light chain. B02C11 recognises both the wild type and Arg2150His factor
 CC VIII light chains. The MAB produced by the cell line of the invention,
 CC KR1X1, specifically recognises the wild type factor VIII light chain.
 CC KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand
 CC factor in a dose dependant manner. The new cell line KR1X 1, is deposited
 CC with the Belgian Coordinated Collections of Micro-organisms, under
 CC accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with
 CC a thrombolytic agent, are useful for the treatment and/or prevention of
 CC haemostasis, coagulation disorder or thrombotic pathologic condition such
 CC as intravascular coagulation, arterial thrombosis, arterial restenosis,
 CC venous thrombosis or arteriosclerosis, and attenuation of coagulation in
 CC a mammal. An effective and safe antithrombotic therapy is provided which
 CC reduces the risk of bleeding in mammals, more particularly in humans
 XX
 XX Sequence 142 AA;

Query Match 100.0%; Score 733; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.9e-42;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
 DB 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
 QY 61 PQQAPRLIYGASTRATGIDPRFSGSGGDTFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 DB 61 PQQAPRLIYGASTRATGIDPRFSGSGGDTFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 QY 121 QGTRLEIKGTVAAPSVFIFFPS 142
 DB 121 QGTRLEIKGTVAAPSVFIFFPS 142

RESULT 2
 AA018877
 ID AA018877 standard; protein; 142 AA.
 XX
 AC AA018877;
 XX
 DT 07-NOV-2002 (first entry)
 XX
 DE Human B02C11 light chain variable region.
 XX
 KW Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
 KW complementarity determining region; antibacterial; antinflammatory.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 FT Region 43..54
 FT /label= CDR1
 FT Region 69..75
 FT /label= CDR2
 FT Region 108..116
 FT /label= CDR3
 XX
 EN EP1222929-A2.
 XX
 PD 17-JUL-2002.
 XX
 PF 11-JAN-2002; 2002EP-00447005.
 XX
 PR 11-JAN-2001; 2001US-0261405P.
 XX
 FA (COLL-) COLLEN RES FOUND VZW D.
 XX
 PI Jacquemin MG, Saint-Remy JR;

XX WPI; 2002-610270/66.
 DR N-PSDB; AAL49255.
 XX
 PT Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 PT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.
 XX
 PS Disclosure; Fig 11; 41pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the light chain variable region of B02C11
 XX
 XX Sequence 142 AA;
 SQ
 Query Match 100.0%; Score 733; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.9e-42;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
 DB 1 METPAQLLFLLLLWLPDTTGEIALTQSPGTLSPGERATLSRCASQSFSSSYLAWYQQK 60
 QY 61 PQQAPRLIYGASTRATGIDPRFSGSGGDTFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 DB 61 PQQAPRLIYGASTRATGIDPRFSGSGGDTFTLTISRLEPEDPAVYCYKYGTSAITFG 120
 QY 121 QGTRLEIKGTVAAPSVFIFFPS 142
 DB 121 QGTRLEIKGTVAAPSVFIFFPS 142
 RESULT 3
 AA93702
 ID AA93702 standard; protein; 235 AA.
 XX
 AC AA93702;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE The kappa chain of immunoglobulin clone 4.1.1.
 XX
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99WO-US030895.
 XX
 PR 23-DEC-1998; 98US-0113647P.
 XX
 PA (PFIZ) PRIZER INC.
 PA (ABGE-) AGENIX INC.
 XX
 PI Hansen DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR WPI; 2000-442647/38.
 DR N-PSDB; AAA46865.
 XX
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
 PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.
 XX PS Claim 3; Fig 1A; 157pp; English.
 XX CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
 CC -4. Antibodies of the invention are composed of a heavy chain variable
 CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
 CC encoded by a human VH3-33 family gene. The modifications are contained in
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
 CC used to up-regulate immune system to up-regulate immunodeficient
 CC disorders
 XX SQ Sequence 235 AA;
 Query Match 93.0%; Score 682; DB 3; Length 235;
 Best Local Similarity 92.3%; Pred. No. 1.2e-38;
 Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 METPAQLLLILLWLPDITGEIATLQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
 DB 1 METPAQLLLILLWLPDITGEIATLQSPGTLSPGERATLSCRASQSPSSSYLAWYQOR 60
 QY 61 PQOAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGTSAITFG 120
 DB 61 PQOAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGTSPWTFG 120
 QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
 DB 121 QGTRLEIKGTVAAPSVFIIPPS 142
 RESULT 4
 ID AAY93729 standard; protein; 235 AA.
 AC AAY93729;
 DT 03-OCT-2000 (first entry)
 DE The kappa chain of immunoglobulin clone 4.1.1.
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 PN WO200037504-A2.
 PD 29-JUN-2000.
 PF 23-DEC-1999; 99WO-US030895.
 PR 23-DEC-1998; 98US-0113647P.
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 DR WPI: 2000-442647/38.
 DR N-PSDB; AAA46893.
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for
 treating, e.g. immune disorders.
 XX PS Claim 3; Fig 22g; 157pp; English.
 XX CC The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
 CC -4. Antibodies of the invention are composed of a heavy chain variable
 CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
 CC encoded by a human VH3-33 family gene. The modifications are contained in
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
 CC used to up-regulate immune system to up-regulate immunodeficient
 CC disorders
 XX SQ Sequence 235 AA;
 Query Match 93.0%; Score 682; DB 3; Length 235;
 Best Local Similarity 92.3%; Pred. No. 1.2e-38;
 Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 METPAQLLLILLWLPDITGEIATLQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
 DB 1 METPAQLLLILLWLPDITGEIATLQSPGTLSPGERATLSCRASQSPSSSYLAWYQOR 60
 QY 61 PQOAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGTSAITFG 120
 DB 61 PQOAPRLLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGTSPWTFG 120
 QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
 DB 121 QGTRLEIKGTVAAPSVFIIPPS 142
 RESULT 5
 ID AAE35884 standard; protein; 235 AA.
 AC AAE35884;
 DT 17-JUN-2003 (first entry)
 DE Human 4.1.1 anti-CTLA-4 antibody kappa chain.
 KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
 KW cancer.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= Signal_peptide
 FT Protein 21..235
 FT /note= "Mature anti-CTLA-4 antibody kappa chain"
 PN EP1262193-A1.
 PD 04-DEC-2002.
 PF 23-MAY-2002; 2002EP-00253652.
 PR 23-MAY-2001; 2001US-0293042P.
 PA (PFIZ) PFIZER PROD INC.
 PI Hanson DC, Mueller EE;
 PI WPI: 2003-131215/13.
 PI N-PSDB; AAD54344.
 PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the

PT preparation of medicament for the treatment of cancer.
XX
PS Disclosure; Fig 1G; 76pp; English.
XX
CC The invention relates to the use of human anti-cytotoxic T lymphocyte
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC cancer, cancer of the anal region, stomach cancer, breast cancer, and
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC The present sequence is human anti-CTLA-4 antibody kappa chain
XX
SQ Sequence 235 AA;
Query Match 93.0%; Score 682; DB 6; Length 235;
Best Local Similarity 92.3%; Pred. No. 1.2e-38;
Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 METPAQLLFLLWLPTTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
Db 1 METPAQLLFLLWLPTTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
QY 121 QGTRLEIKGTVAAPSVFIPIPPS 142
Db 121 QGTRLEIKGTVAAPSVFIPIPPS 142
RESULT 6
ABP71366
ID ABP71366 standard; protein; 235 AA.
XX
AC ABP71366;
XX
DT 28-APR-2003 (first entry)
XX
DE Anti-OPGL-1 antibody kappa light chain.
XX
KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
KW antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Region /note= "IgG2 signal peptide"
FT Region 21..128
FT Region /note= "variable region"
FT Region 129..235
FT Region /note= "constant region"
XX
FN WO2003002713-A2.
XX
PD 09-JAN-2003.
XX
PF 25-JUN-2002; 2002WO-US020181.
XX
PR 26-JUN-2001; 2001US-0301172P.
XX
PA (ABGE-) ABGENIX INC.
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Martin FH, Corvalan JR, Davis GC;
XX
DR WPI; 2003-210262/20.
DR N-PSDB; ABZ59148.
XX
PT New antibodies that interact with osteoprotegerin ligands, useful for
PT treating osteoporosis disorders, e.g. osteoporosis, bone loss from
PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and

osteonecrosis.
XX
PS Claim 1; Fig 4; 144pp; English.
XX
CC The invention relates to antibodies that interact with osteoprotegerin
CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in
CC a biological sample. The antibody, or the pharmaceutical composition
CC comprising the antibody, is also useful for treating osteoporosis disorder,
CC an inflammatory condition with attendant bone loss, an autoimmune
CC condition with attendant bone loss in a patient or rheumatoid arthritis
CC in a patient. In particular, the antibody or composition is useful for
CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'
CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
CC kappa light chain
XX
SQ Sequence 235 AA;
Query Match 90.9%; Score 666; DB 6; Length 235;
Best Local Similarity 90.1%; Pred. No. 1.5e-37;
Matches 128; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 METPAQLLFLLWLPTTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
Db 1 METPAQLLFLLWLPTTGEIALTQSPGTLSPGERATLSRASQSSSYLAHYQOK 60
QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGTSAITFG 120
QY 121 QGTRLEIKGTVAAPSVFIPIPPS 142
Db 121 QGTRLEIKGTVAAPSVFIPIPPS 142
RESULT 7
ADE28481
ID ADE28481 standard; protein; 234 AA.
XX
AC ADE28481;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 24-2-1 full length light chain protein.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX human; light chain; 24-2-1.
OS Homo sapiens.
XX
FN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
DR WPI; 2003-441521/41.
DR N-PSDB; ADE28480.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or

```
PT viral infections.
XX
PS Claim 7; SEQ ID NO 88; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neuropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody full length light chain protein of the invention.
XX
SQ Sequence 234 AA;

Query Match      89.8%; Score 658.5; DB 7; Length 234;
Best Local Similarity 90.1%; Pred. No. 4.7e-37;
Matches 128; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60

QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFVAVYCYQKGTSAITFG 120
DB 61 PGQAPRLIIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFVAVYCYQY-SSLFTFG 119

QY 121 QGTRLEIKGTVAAPSVFIFPPS 142
DB 120 PGTKVDIKRTVAAPSVFIFPPS 141

RESULT 8
AAU74299
ID AAU74299 standard; protein; 236 AA.
XX
AC AAU74299;
XX
XX 12-MAR-2002 (first entry)
XX
DE Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
XX
KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation;
KW graft versus host reaction; immune rejection; intestinal immunity;
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX
OS Homo sapiens.
XX
XX WO200187981-A2.
XX
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-JP004035.
XX
XX 18-MAY-2000; 2000JP-00147116.
XX
XX 30-MAR-2001; 2001JP-00099508.
XX
XX (NISR) JAPAN TOBACCO INC.
XX
XX Tsuji T, Tezuka K, Hori N;
XX
XX WPI; 2002-075313/10.
XX
XX N-PSDB; AAS99475.
XX
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XX New human monoclonal antibody that binds to activation inducible
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT arthritis, multiple sclerosis and inflammation.
XX
PS Claim 30; Page 284-285; 300pp; English.
XX
CC The invention relates to a novel human antibody (I), preferably a human
CC monoclonal antibody which binds to an activation inducible lymphocyte
CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
CC transduction into a cell mediated by AILIM, for modulating proliferation
CC of AILIM-expressing cells, for modulating production of a cytokine from
CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
CC AILIM-expressing cells. (I) is useful for treating, preventing or
CC prophylaxis of delayed type allergy. (I) is useful for treating and
CC preventing various diseases associated with AILIM-mediated costimulatory
CC transduction, and for inhibiting the onset and/or advancement of the
CC diseases. (I) is useful for suppression, prevention and/or treatment of
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC host reaction, graft versus host disease, immune rejection, disorders
CC caused by abnormal intestinal immunity, specifically inflammatory
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC immunorejection due to antigenicity to human, i.e., human anti-mouse
CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
CC AILIM monoclonal antibody amino acid sequences of the invention
XX
SQ Sequence 236 AA;

Query Match      89.8%; Score 658.5; DB 5; Length 236;
Best Local Similarity 89.5%; Pred. No. 4.7e-37;
Matches 128; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
DB 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60

QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFVAVYCYQKGTSAI-TF 119
DB 61 PGQAPGLIIYGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDFVAVYCYQGFSSPMCSF 120

QY 120 QGTRLEIKGTVAAPSVFIFPPS 142
DB 121 CQGTKLEIKRTVAAPSVFIFPPS 143

RESULT 9
AAB47061
ID AAB47061 standard; protein; 143 AA.
XX
AC AAB47061;
XX
XX 08-MAY-2001 (first entry)
XX
XX Light chain variable region VL of KR1X1.
XX
KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;
KW complementarity determining region; CDR; MAb; B02C11.
KW conformational epitope; factor VIII; KR1X1; von Willebrand factor;
KW hemostasis; intravascular coagulation; arterial thrombosis;
KW arterial restenosis; venous thrombosis; arteriosclerosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 43..54 /label= CDR1
XX FT Domain 69..75 /label= CDR2
XX FT
```

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FT Domain 109..118
FT /label= CDR3
XX
XX W0200104269-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-EP006677.
XX
XX 14-JUL-1999; 99GB-00016450.
XX
XX 14-JUL-1999; 99US-0143891P.
XX
XX (LEUV-) LEUVEN RES & DEV VZW.
XX
XX Jacquemin MG, Saint-Remy JR;
XX
XX WPI; 2001-138333/14.
XX
XX N-PSDB; AACB5454.
XX
XX Novel cell lines for producing monoclonal antibodies that bind to a
XX factor involved in hemostasis and coagulation cascade, useful for
XX treating and preventing coagulation disorders.
XX
XX Example 5; Fig 9; 55pp; English.
XX
XX This sequence represents the light chain variable region of the
XX monoclonal antibody (WAB), KR1X1. This MAB produced by the cell line of
XX the invention, specifically recognises the wild type factor VIII light
XX chain. KR1X1 can be used to inhibit the binding of factor VIII to von
XX Willebrand factor in a dose dependant manner. The new cell line KR1X 1.
XX is deposited with the Belgian Coordinated Collections of Micro-organisms,
XX under accession number LMBP 5089CB. KR1X1, or fragments of it, optionally
XX with a thrombolytic agent, are useful for the treatment and/or prevention
XX of hemostasis, coagulation disorder or thrombotic pathologic condition
XX such as intravascular coagulation, arterial thrombosis, arterial
XX restenosis, venous thrombosis or arteriosclerosis, and attenuation of
XX coagulation in a mammal. An effective and safe antithrombotic therapy is
XX provided which reduces the risk of bleeding in mammals, more particularly
XX in humans
XX
XX Sequence 143 AA;
XX
Query Match 89.3%; Score 654.5; DB 4; Length 143;
Best Local Similarity 89.5%; Pred. No. 5.7e-37;
Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSCRASQSVASAYLAWYQOK 60
Qy 61 PQQAPRLIIYGASTRATGIPDRFSGSGSDFTLTISRLEPEDFANVYCKYGTSA-ITF 119
Db 61 PQQAPRLIIYGASTRATGIPDRFSGSGSDFTLTISRLEPEDFANVYCKYGTSA-ITF 119
Qy 120 GQGTRLEIKGTVAAPSVFIPPPS 142
Db 121 GGGTKVEIKRTVAAPSVFIPPPS 143
RESULT 10
AAO18879
ID AAO18879 standard; protein; 143 AA.
XX
XX AAO18879;
XX
XX 07-NOV-2002 (first entry)
XX
XX Human KR1X1 light chain variable region.
XX
XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
XX variable region; factor VIII inhibitor; sepsis; septic shock;
XX thrombus formation; systemic inflammatory response syndrome; CDR;
XX disseminated intravascular coagulation; haemophilia A; immunosuppressive;

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KW complementarity determining region; antibacterial; antiinflammatory.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 43..54
XX /label= CDR1
XX Region 69..75
XX /label= CDR2
XX Region 108..117
XX /label= CDR3
XX
XX EP1222929-A2.
XX
XX 17-JUL-2002.
XX
XX 11-JAN-2002; 2002EP-00447005.
XX
XX 11-JAN-2001; 2001US-0261405P.
XX
XX (COLL-) COLLEN RES FOUND VZW D.
XX
XX Jacquemin MG, Saint-Remy JR;
XX
XX WPI; 2002-610270/66.
XX
XX N-PSDB; AAL49257.
XX
XX Pharmaceutical composition for treating systemic inflammatory response
XX syndrome, sepsis, septic shock and/or thrombus formation in
XX microvasculature in mammals, comprises a partial inhibitor of factor
XX VIII.
XX
XX Disclosure; Fig 13; 41pp; English.
XX
XX The present invention relates to a pharmaceutical composition for the
XX prevention and/or treatment of systemic inflammatory response syndrome
XX (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
XX and disseminated intravascular coagulation in mammals, comprising as an
XX active ingredient a partial inhibitor of factor VIII, in admixture with a
XX carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
XX present sequence is the light chain variable region of KR1X1
XX
XX Sequence 143 AA;
XX
Query Match 89.3%; Score 654.5; DB 5; Length 143;
Best Local Similarity 89.5%; Pred. No. 5.7e-37;
Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSCRASQSVASAYLAWYQOK 60
Qy 61 PQQAPRLIIYGASTRATGIPDRFSGSGSDFTLTISRLEPEDFANVYCKYGTSA-ITF 119
Db 61 PQQAPRLIIYGASTRATGIPDRFSGSGSDFTLTISRLEPEDFANVYCKYGTSA-ITF 119
Qy 120 GQGTRLEIKGTVAAPSVFIPPPS 142
Db 121 GGGTKVEIKRTVAAPSVFIPPPS 143
RESULT 11
AAO18879
ID AAO18879 standard; protein; 233 AA.
XX
XX AAO18879;
XX
XX 03-OCT-2000 (first entry)
XX
XX The kappa chain of immunoglobulin clone 4.8.1.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW

```


KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

OS WO200037504-A2.

PN 29-JUN-2000.

PD 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46867.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.

XX Claim 3; Fig 1B; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the

CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)

CC -4. Antibodies of the invention are composed of a heavy chain variable

CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence

CC encoded by a human VH3-33 family gene. The modifications are contained in

CC CDRI, CDR2 and/or framework regions. The antibodies may be used to

CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity

CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and

CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be

CC used to up-regulate immune system to up-regulate immunodeficient

CC disorders

XX Sequence 233 AA;

Query Match 89.2%; Score 654; DB 3; Length 233;

Best Local Similarity 90.1%; Pred. No. 9.4e-37; Length 233;

Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60

DB 1 METPAQLLFLLLWLPDPTTGTGEIALTQSPGTLSPGERATLSCRT--SVSSSYLAWYQOK 58

QY 61 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 120

DB 59 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 118

QY 121 QGTRLEIKGTVAAPSVFIFPPS 142

DB 119 GGTKEIKRTVAAPSVFIFPPS 140

RESULT 12

AA93731

ID AA93731 standard; protein; 233 AA.

XX AA93731;

XX 03-OCT-2000 (first entry)

XX The kappa chain of immunoglobulin clone 4.8.1.

XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;

XX proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..20
FT /note= "signal peptide"

XX WO200037504-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

XX (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46895.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.

XX Claim 3; Fig 22k; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the

CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)

CC -4. Antibodies of the invention are composed of a heavy chain variable

CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence

CC encoded by a human VH3-33 family gene. The modifications are contained in

CC CDRI, CDR2 and/or framework regions. The antibodies may be used to

CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity

CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and

CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be

CC used to up-regulate immune system to up-regulate immunodeficient

CC disorders

XX Sequence 233 AA;

Query Match 89.2%; Score 654; DB 3; Length 233;

Best Local Similarity 90.1%; Pred. No. 9.4e-37; Length 233;

Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60

DB 1 METPAQLLFLLLWLPDPTTGTGEIALTQSPGTLSPGERATLSCRT--SVSSSYLAWYQOK 58

QY 61 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 120

DB 59 PQQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGTSAITFG 118

QY 121 QGTRLEIKGTVAAPSVFIFPPS 142

DB 119 GGTKEIKRTVAAPSVFIFPPS 140

RESULT 13

AAE35886

ID AAE35886 standard; protein; 233 AA.

XX AAE35886;

XX 17-JUN-2003 (first entry)

XX Human 4.8.1 anti-CTLA-4 antibody kappa chain.

XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;

XX cancer.

OS Homo sapiens.

AC AAY93733;
XX 03-OCT-2000 (first entry)
XX
XX
XX The kappa chain of immunoglobulin clone 6.1.1.
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX Proliferative disorder; cancer; immunodeficient disorder.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /note= "signal peptide"
XX
XX WO200037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US030895.
XX
XX 23-DEC-1998; 98US-0113647P.
XX
XX (PFIZ) PFIZER INC.
XX (ABGE-) ARGENTX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,
XX Corvalan JR;
XX
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46897.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX
XX Claim 3; Fig 22o; 157pp; English.
XX
XX The present sequence represents a kappa chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-FR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDRI, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders
XX
XX Sequence 234 AA;
Query Match 88.7%; Score 650.5; DB 3; Length 234;
Best Local Similarity 89.4%; Pred. NO. 1.6e-36;
Matches 127; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 METPACLLFLLIWLPTTGTGEIATQSPGTLSPGERATLSCRASQSFSSYLAWYQOK 60
DB 1 METPACLLFLLIWLPTTGTGEIATQSPGTLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGSGTDFTLISRLPEPEDFAVYQCKYGTSAITFG 120
DB 60 PGQAPRLIYGVSSTRATGIPDRFSGSGSGTDFTLISRLPEPEDFAVYQCKYGTSAITFG 119
QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
DB 120 PGTKVDIKRTVAAPSVFIIPPS 141

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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 33.3976 Seconds
(without alignments)
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Perfect score: 733
Sequence: 1 MTPAQLLELLLLWLPDRTG.....TFLEIKGVAPSVFIFFPS 142

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Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/pubaa/PCT_NEW_PUB.pep:
3: /cgn2_6/prodata/2/pubaa/US06_NEW_PUB.pep:
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6: /cgn2_6/prodata/2/pubaa/PCTUS_PUBCOMB.pep:
7: /cgn2_6/prodata/2/pubaa/US08_NEW_PUB.pep:
8: /cgn2_6/prodata/2/pubaa/US08_PUBCOMB.pep:
9: /cgn2_6/prodata/2/pubaa/US09A_PUBCOMB.pep:
10: /cgn2_6/prodata/2/pubaa/US09B_PUBCOMB.pep:
11: /cgn2_6/prodata/2/pubaa/US09C_PUBCOMB.pep:
12: /cgn2_6/prodata/2/pubaa/US09_NEW_PUB.pep:
13: /cgn2_6/prodata/2/pubaa/US10A_PUBCOMB.pep:
14: /cgn2_6/prodata/2/pubaa/US10B_PUBCOMB.pep:
15: /cgn2_6/prodata/2/pubaa/US10C_PUBCOMB.pep:
16: /cgn2_6/prodata/2/pubaa/US10_NEW_PUB.pep:
17: /cgn2_6/prodata/2/pubaa/US60_NEW_PUB.pep:
18: /cgn2_6/prodata/2/pubaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	733	100.0	142	14	US-10-044-569B-4
2	682	93.0	235	14	US-10-153-382-7
3	666	90.9	235	12	US-10-180-648-4
4	658.5	89.8	236	9	US-09-859-053-34
5	654.5	89.3	143	14	US-10-044-569B-8
6	654	89.2	233	14	US-10-153-382-11
7	653.5	89.2	236	9	US-09-859-053-38
8	650.5	88.7	234	14	US-10-153-382-15
9	649	88.5	150	10	US-09-782-397-5
10	600.5	81.9	236	11	US-09-833-245-237
11	596	81.3	128	15	US-10-309-764-89
12	590.5	80.6	127	15	US-10-309-762-95
13	590	80.5	384	15	US-10-391-265-804
14	590	80.5	384	15	US-10-391-265-805
15	590	80.5	384	15	US-10-391-265-806

16	590	80.5	384	15	US-10-291-265-807
17	589.5	80.4	234	10	US-09-848-832-4
18	589.5	80.4	234	14	US-10-225-108A-4
19	589.5	80.4	234	15	US-10-461-148-2
20	587.5	80.2	127	15	US-10-309-762-91
21	584.5	79.7	127	15	US-10-309-762-93
22	579	79.0	215	15	US-10-307-724-122
23	574	78.3	307	15	US-10-291-265-332
24	574	78.3	312	15	US-10-291-265-334
25	573.5	78.2	226	10	US-09-453-234-50
26	573.5	78.0	226	10	US-09-453-234-86
27	571.5	78.0	226	10	US-09-453-234-80
28	570.5	77.8	238	14	US-10-216-484-107
29	570.5	77.8	238	14	US-10-384-933-107
30	565	77.1	215	10	US-09-972-656-100
31	564.5	77.0	226	10	US-09-453-234-42
32	564.5	77.0	238	14	US-10-216-484-50
33	564.5	77.0	238	14	US-10-384-933-50
34	561.5	76.6	226	10	US-09-453-234-74
35	559	76.3	141	14	US-10-153-382-23
36	558.5	76.2	224	10	US-09-453-234-52
37	556.5	75.9	119	14	US-10-226-615-4
38	556.5	75.9	119	15	US-10-374-932-4
39	556.5	75.9	226	10	US-09-453-234-72
40	554.5	75.6	226	10	US-09-453-234-38
41	552.5	75.4	224	10	US-09-453-234-44
42	552.5	75.4	224	10	US-09-453-234-76
43	552.5	75.4	224	10	US-09-453-234-78
44	550.5	75.1	224	10	US-09-453-234-40
45	548.5	74.8	129	15	US-10-309-764-105

ALIGNMENTS

RESULT 1

US-10-044-569B-4
; Sequence 4, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)..(162)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (205)..(225)
; OTHER INFORMATION: complementary determining region number two
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (325)..(351)
; OTHER INFORMATION: complementary determining region number three
US-10-044-569B-4

Query Match 100.0%; Score 733; DB 14; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	METPAQLFLLLLWLPDPTGGIATLQSFGTSLSPGERATLSCRASOSFSSSYAWYQQ	60
Db	1	METPAQLFLLLLWLPDPTGGIATLQSFGTSLSPGERATLSCRASOSFSSSYAWYQQ	60
QY	61	PQCAFRLLTYGASTATCIPRFGSGSGDTFTLTISRLPEDPAVYCYKGYTSATFG	120
Db	61	PQCAFRLLTYGASTATCIPRFGSGSGDTFTLTISRLPEDPAVYCYKGYTSATFG	120
QY	121	QGTRLEIKGTVAAPSVFIFFPPS	142
Db	121	QGTRLEIKGTVAAPSVFIFFPPS	142

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RESULT 2
US-10-153-382-7
; Sequence 7, Application US/10153382
; Publication NO. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.11
; SEQ ID NO 7
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-7

```

```

RESULT 3
US-10-180-648-4
; Sequence 4, Application US/10180648
; Publication NO. US20040033535A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPGL
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-4

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Query Match	90.9%	Score 666,	DB 12;	Length 235;
Best Local Similarity	90.1%	Pred. No. 2.7e-49;		
Matches 138; Conservative	6;	Mismatches 8;	Indels 0;	Gaps 0;

Qy	1	METPAQLLFLLWLWLPDTTGEIATLQTSPTGLTSLSPGERATLSCRASQSPSSSYLAWYQOK	60
Db	1	METPAQLLFLLWLWLPDTTGEIIVLTQSPGTLSPGERATLSCRASQSVGRVLAWYQOK	60
Qy	61	PGQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYCKYGTSAITFG	120
Db	61	PGQAPRLIIYGASSTRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYQYGGSSPRTFG	120
Qy	121	QGTREIKNGTVAAPSVFIIPPS	142
Db	121	QGTKEIKRTVAAPSVFIIPPS	142

```

RESULT 4
US-09-859-053-34
Sequence 34, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-34

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RESULT 5
US-10-044-569B-8
; Sequence 8, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical
composition for preventing
inflammatory response syndrome
; TITLE OF INVENTION: Method and/or treating systemic
inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B

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; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/261,405
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (127)..(162)
; OTHER INFORMATION: complementary determining region number one
; NAME/KEY: misc.feature
; LOCATION: (205)..(225)
; OTHER INFORMATION: complementary determining region number two
; NAME/KEY: misc.feature
; LOCATION: (325)..(354)
; OTHER INFORMATION: complementary determining region number three
; US-10-044-569b-8

Query Match      89.3%; Score 654.5; DB 14; Length 143;
Best Local Similarity 89.5%; Pred. No. 1.5e-48;
Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
DB 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYCKYGTSA-ITP 119
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYCKYGTSAITFG 120
QY 120 GQGTREIKGTVAAPSVFIPEPS 142
DB 121 GQGTREIKGTVAAPSVFIPEPS 143

RESULT 6
US-10-153-382-11
; Sequence 11, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-382-11

Query Match      89.2%; Score 654; DB 14; Length 233;
Best Local Similarity 90.1%; Pred. No. 2.8e-48;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
DB 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRT--SVSSSYLAWYQOK 58
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYCKYGTSAITFG 120
DB 59 PGQAPRLIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYCKYGTSAITFG 118
QY 121 GQGTREIKGTVAAPSVFIPEPS 142
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DB 119 GQTKVEIKGTVAAPSVFIPEPS 140

RESULT 7
US-09-859-053-38
; Sequence 38, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-859-053-38

Query Match      89.2%; Score 653.5; DB 9; Length 236;
Best Local Similarity 89.5%; Pred. No. 3.2e-48;
Matches 128; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
DB 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYCKYGTSAI-TF 119
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDTLTISRLEPEDFAVYCYCKYGTSAITFG 120
QY 120 GQGTREIKGTVAAPSVFIPEPS 142
DB 121 GQGTREIKGTVAAPSVFIPEPS 143

RESULT 8
US-10-153-382-15
; Sequence 15, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-382-15

Query Match      88.7%; Score 650.5; DB 14; Length 234;
Best Local Similarity 89.4%; Pred. No. 5.7e-48;
Matches 127; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 METPAQLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
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Db 1 METPAQLLLFWLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAITFG 120
Db 60 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAITFG 119
QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
Db 120 PGTKVDIKRTVAAPSFIIPPS 141

RESULT 9
US-09-782-397-5
; Sequence 5, Application US/09782397
; Publication No. US20030021779A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maity, Pradip K.
; Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,397
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,124
; FILING DATE: 1997-05-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-782-397-5

Query Match 88.5%; Score 649; DB 10; Length 150;
Best Local Similarity 87.7%; Pred. No. 4.7e-48;
Matches 128; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 1 METPAQLLLFWLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOK 60
Db 5 MEFOAQLLLFWLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOK 64
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAITFG 118
Db 65 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAITFG 124
QY 117 ITFGGTRLEIKGTVAAPSVFIIPPS 142

Db 125 ITFGGTRLEIKGTVAAPSVFIIPPS 150

RESULT 10
US-09-833-245-237
; Sequence 237, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 237
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-237

Query Match 81.9%; Score 600.5; DB 11; Length 236;
Best Local Similarity 84.7%; Pred. No. 1.1e-43;
Matches 122; Conservative 3; Mismatches 16; Indels 3; Gaps 2;

QY 1 METPAQLLLFWLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOK 60
Db 1 MEXPAQLLLFWLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSV-SSYLAWYQOK 59
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAITFG 118
Db 60 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSAITFG 119
QY 119 FGQGTREIKGTVAAPSVFIIPPS 142
Db 120 FCXGTRLEIKGTVAAPSVFIIPPS 143

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RESULT 11
US-10-309-764-89
; Sequence 89, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: ABGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-764-89

Query Match      81.3%; Score 596; DB 15; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.4e-43;
Matches 114; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 METPAQLLLFLLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
Db 1 METPAQLLLFLLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSIISALAYQOK 60

QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFG 120
Db 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFG 120

QY 121 QGTRLEIK 128
Db 121 GGTKEIK 128

Query Match      80.6%; Score 590.5; DB 15; Length 127;
Best Local Similarity 89.8%; Pred. No. 4e-43;
Matches 115; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLLFLLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
Db 1 MEAPQALLFLLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60

RESULT 12
US-10-309-762-95
; Sequence 95, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-95

Query Match      80.6%; Score 590.5; DB 15; Length 127;
Best Local Similarity 89.8%; Pred. No. 4e-43;
Matches 115; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLLFLLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
Db 1 MEAPQALLFLLWLPDPTTGTEIATLQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60

RESULT 13
US-10-291-265-804
; Sequence 804, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 804
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-804

Query Match      80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTGEIATLQSPGTLSPGERATLSCRASQSSSYLAAYQOKPGQAPRLIIYGASTRAT 77
Db 167 STGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOKPGQAPRLIIYGASTRAT 226

QY 78 GIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFGGTLRLKGTVAAPSVF 137
Db 227 GIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFGGTLRLKGTVAAPSVF 286

QY 138 IFPPS 142
Db 287 IFPPS 291

RESULT 14
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
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; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

Query Match      80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIIYGASTRAT 77
Db 167 STGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRAT 226

QY 78 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQKGTSAITFGQGTGLEIKGTVAAPSVF 137
Db 227 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQGSPTTFGQGTKVDIKETVAAPSVF 286

QY 138 IFPPS 142
Db 287 IFPPS 291
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RESULT 15
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-806
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Query Match      80.5%; Score 590; DB 15; Length 384;
Best Local Similarity 90.4%; Pred. No. 1.4e-42;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLIIYGASTRAT 77
Db 167 STGEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRAT 226

QY 78 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQKGTSAITFGQGTGLEIKGTVAAPSVF 137
Db 227 GIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQGSPTTFGQGTKVDIKETVAAPSVF 286

QY 138 IFPPS 142
Db 287 IFPPS 291
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Search completed: April 5, 2004, 13:59:13
Job time : 34.3976 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2004, 13:36:42 ; Search time 12.7343 Seconds
(without alignments)
575.678 Million cell updates/sec

Title: US-10-044-569B-4
Perfect score: 733
Sequence: 1 METPAQLLFLLMLPDTTG.....TRLBKGTVAAPSVFIPPS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/2/iaa/5B COMB.pap:*
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- 4: /cgn2_6/prodata/2/iaa/6B COMB.pap:*
- 5: /cgn2_6/prodata/2/iaa/PCITUS COMB.pap:*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	93.0	235	4	US-09-472-087-14
2	682	93.0	235	4	US-09-472-087-65
3	654	89.2	233	4	US-09-472-087-15
4	654	89.2	233	4	US-09-472-087-67
5	650.5	88.7	234	4	US-09-472-087-17
6	650.5	88.7	234	4	US-09-472-087-69
7	649	88.5	150	3	US-08-862-124-5
8	624.5	85.2	134	1	US-08-405-034-4
9	602	82.1	129	2	US-08-480-774A-4
10	574	78.3	116	1	US-08-053-131-183
11	574	78.3	116	2	US-08-096-762-183
12	574	78.3	116	3	US-09-042-353-46
13	574	78.3	116	4	US-08-758-417A-311
14	573.5	78.2	226	4	US-09-456-090A-50
15	573.5	78.2	226	4	US-09-456-090A-86
16	571.5	78.0	226	4	US-09-456-090A-80
17	564.5	77.0	226	4	US-09-456-090A-42
18	561.5	76.6	226	4	US-09-456-090A-74
19	560.5	76.5	234	3	US-09-049-672A-6
20	559	76.3	141	4	US-09-472-087-88
21	558.5	76.2	224	4	US-09-456-090A-52
22	556.5	75.9	226	4	US-09-456-090A-72
23	554.5	75.6	226	4	US-09-456-090A-38
24	552.5	75.4	224	4	US-09-456-090A-44
25	552.5	75.4	224	4	US-09-456-090A-76
26	552.5	75.4	224	4	US-09-456-090A-78
27	550.5	75.1	224	4	US-09-456-090A-40

ALIGNMENTS

RESULT 1

US-09-472-087-14

; Sequence 14, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, ELLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: AX-PFI

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-472-087-14

Query Match 93.0%; Score 682; DB 4; Length 235;

Best Local Similarity 92.3%; Pred. No. 1,2e-54;

Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 METPAQLLFLLMLPDTTGTEIALTQSPGTLSPGGERATLSGRASQSFSSSYLIATYQOK 60

Db 1 METPAQLLFLLMLPDTTGTEIALTQSPGTLSPGGERATLSGRASQSFSSSYLIATYQOK 60

QY 61 PQGAPRLIIYGASRATGIPDRFGSGSGDFTLTISRLEPEDFVYCYCKYGTSAITFG 120

Db 61 PQGAPRLIIYGASRATGIPDRFGSGSGDFTLTISRLEPEDFVYCYCKYGTSAITFG 120

QY 121 QGTRLEIKGTVAAPSVFIPPS 142

Db 121 QGTRLEIKGTVAAPSVFIPPS 142

RESULT 2

US-09-472-087-65

; Sequence 65, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

28 547.5 74.7 235 3 US-08-812-586-16 Sequence 16, Appl

29 547.5 74.7 235 4 US-09-535-832A-17 Sequence 17, Appl

30 547 74.6 235 1 US-08-276-852-153 Sequence 153, App

31 547 74.6 235 1 US-08-899-575-153 Sequence 153, App

32 547 74.6 235 5 PCT-US95-08743-153 Sequence 153, App

33 547 74.6 235 4 US-09-472-087-21 Sequence 21, Appl

34 538.5 73.5 146 4 US-09-472-087-91 Sequence 91, Appl

35 538.5 73.5 146 4 US-09-472-087-89 Sequence 89, Appl

36 531 72.4 141 4 US-08-862-124-14 Sequence 14, Appl

37 531 72.4 141 4 US-09-315-926A-79 Sequence 79, Appl

38 530 72.3 236 4 US-09-472-087-19 Sequence 19, Appl

39 527.5 72.0 142 4 US-09-472-087-92 Sequence 92, Appl

40 526 71.8 142 4 US-08-476-176B-8 Sequence 8, Appl

41 525 71.3 127 2 US-08-127-721A-8 Sequence 8, Appl

42 522.5 71.3 127 3 US-08-485-246A-8 Sequence 16, Appl

43 522.5 71.3 127 3 US-09-472-087-16 Sequence 16, Appl

44 522.5 71.3 139 4 US-09-472-087-16 Sequence 16, Appl

45 522.5 71.3 139 4 US-09-472-087-16 Sequence 16, Appl

```

; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      93.0%; Score 682; DB 4; Length 235;
Best Local Similarity 92.3%; Pred. No. 1.2e-54;
Matches 131; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOR 60

Qy 61 PQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCCQYGTSAITFG 120
Db 61 PQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCCQYGTSAITFG 120

Qy 121 QGTRLEIKGTVAAPSVFIFFPS 142
Db 121 QGTRLEIKGTVAAPSVFIFFPS 142

Query Match      89.2%; Score 654; DB 4; Length 233;
Best Local Similarity 90.1%; Pred. No. 4.1e-52;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 3
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15

Query Match      89.2%; Score 654; DB 4; Length 233;
Best Local Similarity 90.1%; Pred. No. 4.1e-52;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRATLSRT--SVSSSYLANWYQOK 58

Qy 61 PQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCCQYGTSAITFG 120
Db 59 PQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCCQYGTSAITFG 118

Qy 121 QGTRLEIKGTVAAPSVFIFFPS 142
Db 119 GGTKEIKRTVAAPSVFIFFPS 140

RESULT 5
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-17

Query Match      89.2%; Score 654; DB 4; Length 233;
Best Local Similarity 90.1%; Pred. No. 4.1e-52;
Matches 128; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSFSSSYLANWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRATLSRT--SVSSSYLANWYQOK 58

Qy 61 PQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCCQYGTSAITFG 120
Db 59 PQAPRLIIYGASTRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYCCQYGTSAITFG 118

Qy 121 QGTRLEIKGTVAAPSVFIFFPS 142
Db 119 GGTKEIKRTVAAPSVFIFFPS 140
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US-09-472-087-17

Query Match 88.7%; Score 650.5; DB 4; Length 234;
 Best Local Similarity 89.4%; Pred. No. 8.6e-52;
 Matches 127; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
 QY 1 METPAQLLLFLLLLWLPDITGTEIATQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
 DB 1 METPAQLLLFLLLLWLPDITGTEIATQSPGTLSPGERATLSCRASQSV-SSYLAWYQOK 59
 QY 61 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
 DB 60 PQAPRLIYGVSRTATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGISPFTFG 119
 QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
 DB 120 PGTKVDIKRTVAAPSVFIIPPS 141

RESULT 6

US-09-472-087-69
 ; Sequence 69, Application US/09472087
 ; Patent No. 6682736
 ; GENERAL INFORMATION:
 ; APPLICANT: HANSON, DOUGLAS C.
 ; APPLICANT: NEVEU, MARK J.
 ; APPLICANT: MUELLER, EILLEN E.
 ; APPLICANT: HANKE, JEFFREY H.
 ; APPLICANT: GILMAN, STEVEN C.
 ; APPLICANT: DAVIS, C. GEORFFREY
 ; APPLICANT: CORVALAN, JOSE R.
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
 ; FILE REFERENCE: ABX-PFI
 ; CURRENT APPLICATION NUMBER: US/09/472,087
 ; CURRENT FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,647
 ; PRIOR FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 69
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-472-087-69

Query Match 88.7%; Score 650.5; DB 4; Length 234;
 Best Local Similarity 89.4%; Pred. No. 8.6e-52;
 Matches 127; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 METPAQLLLFLLLLWLPDITGTEIATQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
 DB 1 METPAQLLLFLLLLWLPDITGTEIATQSPGTLSPGERATLSCRASQSV-SSYLAWYQOK 59
 QY 61 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
 DB 60 PQAPRLIYGVSRTATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGISPFTFG 119
 QY 121 QGTRLEIKGTVAAPSVFIIPPS 142
 DB 120 PGTKVDIKRTVAAPSVFIIPPS 141

RESULT 7

US-08-862-124-5
 ; Sequence 5, Application US/08862124
 ; Patent No. 6207153
 ; GENERAL INFORMATION:
 ; APPLICANT: Dan, Michael D.
 ; APPLICANT: Maiti, Pradip K.
 ; APPLICANT: Kaplan, Howard A.
 ; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
 ; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
 ; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
 ; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

; TITLE OF INVENTION: DETECTION OF CANCERS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster LLP
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/862,124
 ; FILING DATE: 22-MAY-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lehnhardt, Susan K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 31608-20001.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 813-5600
 ; TELEFAX: (650) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 150 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-862-124-5

Query Match 88.5%; Score 649; DB 3; Length 150;
 Best Local Similarity 87.7%; Pred. No. 7.1e-52;
 Matches 128; Conservative 6; Mismatches 8; Indels 4; Gaps 1;
 QY 1 METPAQLLLFLLLLWLPDITGTEIATQSPGTLSPGERATLSCRASQSFSSSYLAWYQOK 60
 DB 5 MEFOAQLLLFLLLLWLPDITGDIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOK 64
 QY 61 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCKYGTSAITFG 120
 DB 65 PQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYGISPFTFG 124
 QY 117 ITFGQTRLEIKGTVAAPSVFIIPPS 142
 DB 125 ITFGGIRKIVKRTVAAPSVFIIPPS 150

RESULT 8

US-08-405-034-4
 ; Sequence 4, Application US/08405034
 ; Patent No. 5744585
 ; Patent No. 5744585 5712371
 ; GENERAL INFORMATION:
 ; APPLICANT: Medenica, Rajko D.
 ; APPLICANT: Mukerjee, Sonjoy
 ; TITLE OF INVENTION: Human Monoclonal Antibody Against Lung
 ; TITLE OF INVENTION: Carcinoma
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dewitt Ross & Stevens, S.C.
 ; STREET: 8000 Excelsior Drive, Suite 401
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: USA
 ; ZIP: 53717-1914
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,034
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34656.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-405-034-4

Query Match      85.2%; Score 624.5; DB 1; Length 134;
Best Local Similarity 91.8%; Pred. No. 1e-49;
Matches 123; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
DB 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSPSRFLAWYQOK 60

QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSA-ITF 119
DB 61 PGQAPSLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYQSSARYTF 120

QY 120 GQGTLEIKGTVA 133
DB 121 GQGTLEIKGTVA 134

RESULT 9
US-08-480-774A-4
; Sequence 4, Application US/08480774A
; Patent No. 5852186
; GENERAL INFORMATION:
; APPLICANT: MARASCO, Wayne A.
; APPLICANT: SODROSKI, Joseph G.
; APPLICANT: HASELTINE, William A.
; APPLICANT: POSNER, Marshall R.
; TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
; TITLE OF INVENTION: ANTI-gp 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSQ for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/480,774A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/400,674
; FILING DATE: 08-MAR-1995
; APPLICATION NUMBER: 07/804,652
; FILING DATE: 10-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 41450-FWC-DIV
; FILING DATE:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-480-774A-4

Query Match      82.1%; Score 602; DB 2; Length 129;
Best Local Similarity 90.6%; Pred. No. 1e-47;
Matches 116; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 METPAQLFLLLWLPDPTTGEIALTQSPGTLSPGERATLSCRASQSPSSSYLAWYQOK 60
DB 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSVSSRYLAWYQOK 60

QY 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQKGTSAITFG 120
DB 61 PGQAPRLIIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYCOYDNSVCTFG 120

QY 121 QGTLEIK 128
DB 121 QGTLEIK 128

RESULT 10
US-08-053-131-183
; Sequence 183, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/053,131
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
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;
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-131-183

Query Match          78.3%; Score 574; DB 1; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 METPAQLFLLWLPTTGTGEIALTQSPGTLSLSPGERATLSRASQSFSSSYLAWYQOK 60
DB 1 METPAQLFLLWLPTTGTGEIVLTQSPGTLSLSPGERATLSRASQSVSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYKGS 115
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYKGS 115

RESULT 11
US-08-096-762-183
; Sequence 183, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-096-762-183

Query Match          78.3%; Score 574; DB 2; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 METPAQLFLLWLPTTGTGEIALTQSPGTLSLSPGERATLSRASQSFSSSYLAWYQOK 60
DB 1 METPAQLFLLWLPTTGTGEIVLTQSPGTLSLSPGERATLSRASQSVSSSYLAWYQOK 60
QY 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYKGS 115
DB 61 PGQAPRLIYGASTRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCYQYKGS 115

RESULT 12
US-09-042-353-46
; Sequence 46, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-353-46

Query Match 78.3%; Score 574; DB 3; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSGRASQSVSSSYLAWYQOK 60

Qy 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCQYKTS 115
Db 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCQYKTS 115

RESULT 13
US-08-758-417A-311
Sequence 311, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 311:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 311:
US-08-758-417A-311

Query Match 78.3%; Score 574; DB 4; Length 116;
Best Local Similarity 95.7%; Pred. No. 3.4e-45;
Matches 110; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 METPAQLLLLLWLPDPTTGEIALTQSPGTLSPGERATLSGRASQSPSSSYLAWYQOK 60
Db 1 METPAQLLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSGRASQSVSSSYLAWYQOK 60

Qy 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCQYKTS 115
Db 61 PGQAPRLIYGASTRATGIDPRFSGSGSGTDFTLTISRLEPEDFAVYQCQYKTS 115

RESULT 14
US-09-456-090A-50
Sequence 50, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkira, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 50
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match 78.2%; Score 573.5; DB 4; Length 226;
Best Local Similarity 91.9%; Pred. No. 8.2e-45;
Matches 113; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLLIYGASTRATGIP 80
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP 60
QY 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVPFIF 139
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVPFIF 120
QY 140 PPS 142
DB 121 PPS 123

RESULT 15
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buéchlér, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match 78.2%; Score 573.5; DB 4; Length 226;
Best Local Similarity 91.9%; Pred. No. 8.2e-45;
Matches 113; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 21 EIALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQKPGQAPRLLIYGASTRATGIP 80
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP 60
QY 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVPFIF 139
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYKGTGTS-AITFGQGTRLKIKGTVAAPSVPFIF 120
QY 140 PPS 142
DB 121 PPS 123

Search completed: April 5, 2004, 13:44:08
Job time : 12.7343 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 12.6701 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-6
Perfect score: 837
Sequence: 1 MDWTWRILFLVAAATGAHSQ.....GVTSHYPDYWGRTLVTVSS 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	606.5	72.5	135	2 S49530	anti-Sm antibody V
2	591.5	70.7	171	2 S23623	Ig heavy chain V r
3	550	65.7	117	2 S18551	Ig heavy chain V r
4	549.5	65.7	136	2 S31600	Ig heavy chain V r
5	548	65.5	117	1 HVHU35	Ig heavy chain pre
6	540	64.5	117	2 S31680	Ig heavy chain V r
7	523.5	62.5	132	2 S31596	Ig heavy chain V r
8	521	62.2	160	2 PLO105	anti-PR2 erythrocy
9	517	61.8	148	2 S29257	Ig heavy chain V r
10	515	61.5	142	2 S19245	Ig heavy chain pre
11	505	60.3	129	2 S46393	Ig heavy chain V r
12	502	60.0	123	2 D33548	Ig heavy chain V-1
13	498	59.5	142	2 A32483	Ig heavy chain V r
14	493	58.9	117	2 S18553	Ig heavy chain V r
15	491	58.7	134	2 S21516	Ig heavy chain V r
16	490.5	58.6	118	2 S36265	Ig heavy chain V r
17	489	58.4	627	2 S14683	Ig mu chain precu
18	486	58.1	117	1 HVHUHG	Ig heavy chain pre
19	482.5	57.6	143	1 E1HUND	Ig heavy chain pre
20	477	57.0	117	2 S18554	Ig heavy chain V r
21	474	56.8	131	2 S21924	Ig gamma chain pre
22	465	55.6	117	2 PTH0371	Ig heavy chain pre
23	464.5	55.5	139	1 MHMS18	Ig heavy chain pre
24	462.5	55.3	137	2 C41287	Ig heavy chain pre
25	460	55.0	117	2 S18554	Ig heavy chain V r
26	456	54.5	138	1 HVMS7	Ig heavy chain pre
27	454	54.2	104	2 S69899	Ig heavy chain V r
28	453.5	54.2	110	2 PH1669	Ig heavy chain V r
29	450.5	53.8	135	2 A30577	Ig heavy chain pre

30 450 53.8 138 2 E32513 Ig heavy chain pre
31 447 53.4 111 2 S21925 Ig heavy chain V r
32 446 53.3 98 2 S26938 Ig heavy chain V r
33 443 52.9 121 2 S20783 Ig heavy chain V r
34 439.5 52.5 137 1 G2MS43 Ig heavy chain pre
35 438.5 52.4 116 2 S31698 Ig heavy chain V r
36 438 52.3 98 2 S26912 Ig heavy chain pre
37 438 52.3 109 2 PH1668 Ig heavy chain V r
38 437.5 52.3 137 2 F29380 Ig heavy chain pre
39 437.5 52.3 474 1 G2MS11 Ig gamma-2b chain
40 436.5 52.2 116 2 S31667 Ig heavy chain V r
41 435.5 52.0 137 2 H32513 Ig heavy chain pre
42 435 52.0 127 2 S34014 Ig heavy chain V r
43 434 51.9 126 2 I44151 Ig heavy chain V r
44 433.5 51.8 137 2 E29380 Ig heavy chain pre
45 433.5 51.8 459 2 S37483 Ig gamma-2a chain

ALIGNMENTS

RESULT 1

S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID:G560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:334-117/Domain: immunoglobulin homology <IMW>

Query Match 72.5%; Score 606.5; DB 2; Length 135;
Best Local Similarity 77.6%; Pred. No. 4.9e-46;
Matches 121; Conservative 6; Mismatches 8; Indels 21; Gaps 3;

QY 1 MDWTWRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTQYSASGHFTA 60
DB 1 MDWTWRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50
QY 61 YSVHWVQAPQGGLEWNGRINPNSGATDYAHKFGQRTVMSRDTISISTAYNELSLRSDDT 120
DB 51 YVHWVQAPQGGLEWNGRINPNSGGTNYAQKFGRTVTRDTISISTAYNELSLRSDDT 110
QY 121 AMYTCARADNYFDIVTGVTSHTSYFDYWGRTLVTVSS 156
DB 111 AVYICARAR-----TGY-----NWYGGTLVTVSS 135

RESULT 2

S23623
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23623
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:Cross-references: EMBL:X59702; NID:G32010; PIDN:CAA42223.1; PID:G32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 591.5; DB 2; Length 171;
Best Local Similarity 75.0%; Pred. No. 1.3e-44;
Matches 117; Conservative 9; Mismatches 19; Indels 11; Gaps 2;

QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 120

DB 51 YQHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 110

QY 121 AMYTCARADNFDIVTGYTSHYFDYWGRTLVTVSS 156

DB 111 AVYICARWDAFDI-----WGQGITVTVSS 145

RESULT 3

S18551

Ig heavy chain V region precursor (VI-2) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999

C:Accession: S18551; S23625

R:Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H

EMBO J. 10, 3641-3645, 1991

A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl

A:Reference number: S18551; MUID:92037524; PMID:1935893

A:Accession: S18551

A:Molecule type: DNA

A:Residues: 1-117 <SH>

A:CROSS-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23625

A:Molecule type: DNA

A:Residues: 1-117 <OLE>

A:CROSS-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 550; DB 2; Length 117;

Best Local Similarity 83.5%; Pred. No. 3.6e-41;

Matches 106; Conservative 4; Mismatches 7; Indels 10; Gaps 1;

QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 120

DB 51 YQHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 110

QY 121 AMYTCAR 127

DB 111 AVYICAR 117

RESULT 4

S31600

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31600

R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CDU>
A:CROSS-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 549.5; DB 2; Length 136;

Best Local Similarity 69.9%; Pred. No. 4.7e-41;

Matches 109; Conservative 12; Mismatches 14; Indels 21; Gaps 2;

QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 120

DB 51 YDINWVRQATGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 110

QY 121 AMYTCARADNFDIVTGYTSHYFDYWGRTLVTVSS 156

DB 111 AVYICARWDAFDI-----WGQGITVTVSS 135

RESULT 5

HVHU35

Ig heavy chain precursor V region (V35) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000

C:Accession: S00476; S34013

R:Natsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuh

EMBO J. 7, 1047-1051, 1988

A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain 1

A:Reference number: S00476; MUID:88296408; PMID:2841108

A:Accession: S00476

A:Molecule type: DNA

A:Residues: 1-117 <MATS>

A:CROSS-references: EMBL:X07448; NID:g33104; PIDN:CA856703.1; PID:g6002173

A>Note: the authors translated the codon AGT for residue 89 as Met

R:Mariette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34013

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 20-116 <MAR>

C:Genetics:

A:Gene: GDB:IGHV@

A:CROSS-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 548; DB 1; Length 117;

Best Local Similarity 82.7%; Pred. No. 5.4e-41;

Matches 105; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

DB 1 MDWTWRIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 120

DB 51 YQHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRSDDT 110

QY 121 AMYTCAR 127

DB 111 AVYICAR 117

Db 51 YMHVVRQAPGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 110
QY 121 AMYYCAR 127
Db 111 VVYYCAR 117

RESULT 6

S31680
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31680
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31680
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <CUI>
A:Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 64.5%; Score 540; DB 2; Length 117;
Best Local Similarity 81.1%; Pred. No. 2.7e-40;
Matches 103; Conservative 7; Mismatches 7; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 120
Db 51 YMHVVRQAPGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 110
QY 121 AMYYCAR 127
Db 111 VVYYCAR 117

RESULT 7

S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.58%; Score 523.5; DB 2; Length 132;
Best Local Similarity 67.3%; Pred. No. 8.4e-39;
Matches 105; Conservative 11; Mismatches 15; Indels 25; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 120

Db 51 YDIDWVRQATGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 110
QY 121 AMYYCARADNYFDIVTGYTSHYFDYWGRTVTVSS 156
Db 111 AVYYLAKA-----PAWGQGTMTVTVSS 131

RESULT 8

PL0105
anti-Pr2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C:Accession: PL0105
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J:Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec

A:Reference number: PL0106; MUID:89235583; PMID:2541221
A:Accession: PL0105
A:Molecule type: mRNA
A:Residues: 1-160 <SIL>
A:Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blc
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; hemagglutinin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:49-54/Region: complementarity-determining 1
F:69-84/Region: complementarity-determining 2
F:118-131/Domain: D region <DRG>
F:132-144/Domain: J4 segment <JSG>
F:145-160/Domain: C region <CRG>

Query Match 62.2%; Score 521; DB 2; Length 160;
Best Local Similarity 67.9%; Pred. No. 1.7e-38;
Matches 106; Conservative 8; Mismatches 30; Indels 12; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 120
Db 51 YGISWVRQAPGQGLEWNGRINPNSGGTNYAQKFGQRTVSTRTDTSISTAYMELSLRSDDT 110
QY 121 AMYYCARADNYFDIVTGYTSHYFDYWGRTVTVSS 156
Db 111 AVYYCARAPGYCSGGGCTRGD--DYWGQGLTVTVSS 144

RESULT 9

S29257
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouchane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment
A:Reference number: S29257; MUID:92362614; PMID:1499555
A:Accession: S29257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:S42403; NID:g253699; PIDN:AA22940.1; PID:g253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 517; DB 2; Length 148;
Best Local Similarity 65.4%; Pred. No. 3.5e-38;
Matches 104; Conservative 15; Mismatches 26; Indels 14; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKPGASVKVSKTSKGTSGYFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKASGYT-----PAM 50
Qy 61 YSVHWVROAPGQGLEWNGRINPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDT 120
Db 51 YALHWVROAPGQGLEWNGHISVADGKTKYSQFQDRVITRDTISATTAYMEVGRLSRSDT 110
Qy 121 AMYICARADNYFDIVTGY---TSHYFDYWGRTGLTVSS 156
Db 111 AVTYCARSPR-INMVGVLITTPMPFDSMGQGLTVIVSS 148

RESULT 10

S19245
Ig heavy chain precursor V region (10P1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S19245
R:Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
EMBO J. 11, 603-609, 1992
A:Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure
A:Reference number: S19245; MUID:92164649; PMID:1537339
A:Accession: S19245
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-142 <KIR>
A:Cross-references: EMBL:X59906; NID:g37791; PIDN:CAA42547.1; PID:g37792
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 61.5%; Score 515; DB 2; Length 142;
Best Local Similarity 64.7%; Pred. No. 5e-38;
Matches 101; Conservative 20; Mismatches 21; Indels 14; Gaps 3;

Qy 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKASGYTFTG-----FTS 60
Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKASGYT-----FTS 50
Qy 61 YSVHWVROAPGQGLEWNGRINPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDT 120
Db 51 YANWVROAPGQGLEWNGHISVADGKTKYSQFQDRVITRDTISATTAYMEVGRLSRSDT 110
Qy 121 AMYICARADNYFDIVTGYTSHYFDYWGRTGLTVSS 156
Db 111 AVTYCARA--YTLWMTAVT--HFDVWGQGLTVIVSS 142

RESULT 11

S46393
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FTG>
A:Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 505; DB 2; Length 129;
Best Local Similarity 72.7%; Pred. No. 3.4e-37;
Matches 101; Conservative 8; Mismatches 18; Indels 12; Gaps 2;
Qy 20 QVQLVQSGAEVKKPGASVKVCKTSYGNFTGYSASGHIFTAYSVHWVROAPGQGLEWNGR 79

Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTG-----YMHVWVROAPGQGLEWNGW 50
Qy 80 INPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTAMYYCARADNYFDIVTGYT 139
Db 51 INPNSGATNYAQKFGQGVMTMSRDTISITAYMELSLRSLRSDDTAVVYCARDASVYYDSSGY 110
Qy 140 S--HYFDYWGRTGLTVSS 156
Db 111 SANYYDMVGKGTIVTVSS 129

RESULT 12

D33548
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A:Reference number: A33548; MUID:199345575; PMID:2503826
A:Accession: D33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.0%; Score 502; DB 2; Length 123;
Best Local Similarity 72.5%; Pred. No. 5.9e-37;
Matches 100; Conservative 10; Mismatches 12; Indels 16; Gaps 3;

Qy 20 QVQLVQSGAEVKKPGASVKVCKTSYGNFTGYSASGHIFTAYSVHWVROAPGQGLEWNGR 79
Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTG-----HYMHVROAPGQGLEWNGW 50
Qy 80 INPNSGATDYAHKFGQGVMTMSRDTISITAYMELSLRSLTSDTAMYYCARADNYFDIVTGYT 139
Db 51 INPNSGATNYAEKFGQGVMTTRDTISINTAYMELSLRSLRSDDTAVVYCARAS-----YCGYD 105
Qy 140 SHY--FDYWGRTGLTVSS 156
Db 106 CYFFDYWGQGLTVIVSS 123

RESULT 13

A32483
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
R:Larick, J.W.; Danielson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck,
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells us
A:Reference number: A32483; MUID:89273586; PMID:2499327
A:Accession: A32483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <LAR>
A:Cross-references: GB:M26463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 59.5%; Score 498; DB 2; Length 142;
Best Local Similarity 67.8%; Pred. No. 1.5e-36;
Matches 103; Conservative 10; Mismatches 19; Indels 20; Gaps 4;

Qy 10 LVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSYGNFTGYSASGHIFTAYSVHWVROA 69
Db 1 LLVAPGAHSQVQLVQSGAEVKKPGASVKVCKASGYTFTN-----YYMEVROA 50

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QY 70 PQGLEWGRINPNSGATDYAHKFGQRTVMSRDTSISTAYMELSLRLTSDDTAMYYCAR-- 127
Db 51 PQGLEWGIINPSGNSINACKFGQRTVMTREDTSTVYMELSLRLSREDAVYYCAREK 110
QY 128 -ADNYFD--IVTGYTSHYFDYNGRGLTVTVSS 156
Db 111 LATTIFGVLIITG-----MDYWGQGLTVTVSS 137

RESULT 14
S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C/Accession: S18553; S26916
R/Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3643-3645, 1991
A/Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A/Reference number: S18551; MUID:92037524; PMID:1935893
A/Accession: S18553
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-117 <SHI>
A/Cross-references: EMBL:X62109
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26916
A/Molecule type: DNA
A/Residues: 20-117 <TOM>
A/Cross-references: EMBL:Z12327; NID:G32871; PIDN:CAA78197.1; PID:G32872
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 493; DB 2; Length 117;
Best Local Similarity 74.8%; Pred. No. 3.4e-36;
Matches 95; Conservative 9; Mismatches 13; Indels 10; Gaps 1;

QY 1 MDWTWRLFLVAATGAHSQVQLVQSGAEVKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAATGVHSQVQLVQSGAEVKPGASVKVCKASGYT-----FTS 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSISTAYMELSLRLTSDDT 120
Db 51 YAHWHVRQAPGQRLWNGWGNAGNGNTKYSQKFGQRTITRDTASTAYMELSLRLSREDT 110
QY 121 AMYYCAR 127
Db 111 AVYYCAR 117

RESULT 15
S21916
Ig heavy chain V region precursor - human (fragment)
N/Alternate names: rheumatoid factor
C/Species: Homo sapiens (man)
C/Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 21-Jan-2000
C/Accession: S21916
R/Mierau, R.; Gause, A.; Kueppers, R.; Michels, M.; Mageed, R.A.; Jefferis, R.; Genth, E
submitted to the EMBL Data Library, July 1991
A/Description: A Human monoclonal IgA rheumatoid factor using the Vk(IV) light chain gen
A/Reference number: S21916
A/Accession: S21916
A/Molecule type: mRNA
A/Residues: 1-134 <MIE>
A/Cross-references: EMBL:X61124; NID:G33286; PIDN:CAA43436.1; PID:G33287
C/Superfamily: immunoglobulin V region; immunoglobulin homology
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C/Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 491; DB 2; Length 134;
Best Local Similarity 59.6%; Pred. No. 5.9e-36;
Matches 93; Conservative 19; Mismatches 22; Indels 22; Gaps 2;

QY 1 MDWTWRLFLVAATGAHSQVQLVQSGAEVKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAATGAHSQVQLVQSGSELKPGASVKVCKASGYTFIN----- 50
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSISTAYMELSLRLTSDDT 120
Db 51 YALNWLRLQAPGQGLEWMGWINTNTGKTAQAFTGRFVFLSDTSVSTTTLQISSLRKREDT 110
QY 121 AMYYCARADNYFDIVTGYTSHYFDYNGRGLTVTVSS 156
Db 111 AVYFCAR-----DRWNDYWGQGTQVTVSS 134

Search completed: April 5, 2004, 13:43:02
Job time : 12.6701 secs
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	548	65.5	117	1	HV1G HUMAN	P23083	homo sapien
2	489.5	58.5	147	1	HV1C HUMAN	P01744	homo sapien
3	486	58.1	117	1	HV1B HUMAN	P01743	homo sapien
4	464.5	55.5	139	1	HV07 MOUSE	P01751	mus musculus
5	456	54.5	138	1	HV48 MOUSE	P03980	mus musculus
6	439.5	52.5	137	1	HV11 MOUSE	P01755	mus musculus
7	416	49.7	140	1	HV02 MOUSE	P01746	mus musculus
8	413	49.3	136	1	HV15 MOUSE	P01759	mus musculus
9	402	48.0	117	1	HV05 MOUSE	P01753	mus musculus
10	398	47.6	117	1	HV04 MOUSE	P01748	mus musculus
11	396	47.3	117	1	HV06 MOUSE	P01750	mus musculus
12	381	45.5	117	1	HV49 MOUSE	P06328	mus musculus
13	380	45.4	117	1	HV10 MOUSE	P01754	mus musculus
14	380	45.4	120	1	HV03 MOUSE	P01747	mus musculus
15	373.5	44.6	120	1	HV30 MOUSE	P06329	mus musculus
16	373	44.6	117	1	HV14 MOUSE	P01758	mus musculus
17	372	44.4	117	1	HV05 MOUSE	P01749	mus musculus
18	372	44.4	117	1	HV52 MOUSE	P06327	mus musculus
19	371	44.3	117	1	HV13 MOUSE	P01757	mus musculus
20	365	43.6	117	1	HV12 MOUSE	P01756	mus musculus
21	361.5	43.2	118	1	HV51 MOUSE	P06330	mus musculus
22	358	42.8	125	1	HV1F HUMAN	P06326	homo sapien
23	347	41.5	117	1	HV1A HUMAN	P01742	homo sapien
24	347	41.5	121	1	HV01 MOUSE	P01745	mus musculus
25	343.5	41.0	114	1	HV00 MOUSE	P01741	mus musculus
26	332.5	39.7	120	1	HV1H HUMAN	P80421	homo sapien
27	328	39.2	121	1	HV1J HUMAN	P01771	homo sapien
28	326.5	39.0	124	1	HV1D HUMAN	P01760	homo sapien
29	326.5	39.0	136	1	HV1S MOUSE	P01783	mus musculus
30	323	38.6	142	1	HV01 RAT	P04805	rattus norv
31	320.5	38.3	124	1	HV1E HUMAN	P01761	homo sapien
32	316.5	37.8	119	1	HV38 MOUSE	P01808	mus musculus
33	315.5	37.7	119	1	HV37 MOUSE	P01807	mus musculus

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00529; AAA38170.1; -
DR PIR; A90809; MHMS18.
DR PDB; 1A6U; 27-MAY-98.
DR PDB; 1A6W; 15-JUL-98.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
KW SIGNAL 1 19 IG HEAVY CHAIN V REGION B1-8/186-2.
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 143
FT NON_TER 139
FT SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;
Query Match 55.5%; Score 464.5; DB 1; Length 139;
Best Local Similarity 57.7%; Pred. No. 1.7e-38;
Matches 90; Conservative 20; Mismatches 29; Indels 17; Gaps 2;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVSCKTSYNYFTGYSASGHIFTA 60
DB 1 MGWSYILFLVATATGVHSQVQLQPGAEIVKPGASVKLSCKSGYT-----FTS 50
QY 61 YSVHWVQAPGQGLEWGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDT 120
DB 51 YNHWVQAPGQGLEWIGRIDPNSGCTKNEKSKATLTVDKPSSTAYMQLSSLTSDS 110
QY 121 AMYICARADNYFDIVGTYSHTFYDYGRTLTIVSS 156
DB 111 AVYICARYDY-----YGSYFDYWGQGTTLTVSS 139
Query Match 55.5%; Score 464.5; DB 1; Length 139;
Best Local Similarity 57.7%; Pred. No. 1.7e-38;
Matches 90; Conservative 20; Mismatches 29; Indels 17; Gaps 2;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVSCKTSYNYFTGYSASGHIFTA 60
DB 1 MGWSYILFLVATATGVHSQVQLQPGAEIVKPGASVKLSCKSGYT-----FTS 50
QY 61 YSVHWVQAPGQGLEWGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDT 120
DB 51 YNHWVQAPGQGLEWIGRIDPNSGCTKNEKSKATLTVDKPSSTAYMQLSSLTSDS 110
QY 121 AMYICARADNYFDIVGTYSHTFYDYGRTLTIVSS 156
DB 111 AVYICARYDY-----YGSYFDYWGQGTTLTVSS 139
RESULT 5
HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=84248078; PubMed=6429663;
RX Gilliam A.C., Shen A., Richards J.B., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an Igo-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20 IG HEAVY CHAIN V REGION TEPC 1017.
FT CHAIN 21 138
FT DOMAIN 21 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 138
FT DISULFID 41 115
FT NON_TER 138
FT SEQUENCE 138 AA; 15576 MW; 748157F4C6907B8E CRC64;
Query Match 54.5%; Score 456; DB 1; Length 138;
Best Local Similarity 55.8%; Pred. No. 1.1e-37;
Matches 87; Conservative 23; Mismatches 28; Indels 18; Gaps 2;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVSCKTSYNYFTGYSASGHIFTA 60
DB 1 MGWSYILFLVATATGVHSQVQLQPGAEIVKPGASVKLSCKSGYT-----ASGHTFTN 50
QY 61 YSVHWVQAPGQGLEWGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLTSDDT 120
DB 51 YNHWVQAPGQGLEWIGRIDPNSGCTKNEKSKATLTVDKSSSTAYMQLSSLTPEEF 110
QY 121 AMYICARADNYFDIVGTYSHTFYDYGRTLTIVSS 156
DB 111 AVYICARSDGYD-----WFWYWGQGTTLTVSS 138
RESULT 6
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region 843 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RX Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA


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CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
CC (NPE ANTIBODIES).
CC -----
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CC -----
DR EMBL; J00539; AAA381172.1; -
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137
FT SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;
Query Match 52.5%; Score 439.5; DB 1; Length 137;
Best Local Similarity 55.1%; Pred. No. 4.6e-36;
Matches 86; Conservative 18; Mismatches 33; Indels 19; Gaps 2;
QY 1 MDWTWILFLVAATAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MGWSCIIMFLAATATGVHSEVQLQPGAEFVPPGASVKLSCKASGYT-----FTS 50
QY 61 YSVHWYRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDT 120
DB 51 YLMHWYNQRPGRGLEWIGRIDPNSGGTTTNEHFRSKATLTIDKPSSTAYMQLSLTSDS 110
QY 121 AMYTCARADNYFDIVGTYSHYFDYWGRTLVTVSS 156
DB 111 AVYTCARY-----RLGRYFDYWGQGTTLTVSS 137
RESULT 7
HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -/- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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CC -----
DR EMBL; J00493; AAA381128.1; -
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
Query Match 49.7%; Score 416; DB 1; Length 140;
Best Local Similarity 50.6%; Pred. No. 9.3e-34;
Matches 79; Conservative 29; Mismatches 32; Indels 16; Gaps 2;
QY 1 MDWTWILFLVAATAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MGWSCIIMFLAATATGVHSEVQLQPGAEFVPPGASVKLSCKASGYT-----FTS 50
QY 61 YSVHWYRQAPGQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTISITAYMELSLTSDT 120
DB 51 YGMWVQKQRPQGLEWIGINPQNGVINYNEKFGKTLTVDKSSSTAYMQLSLTSDS 110
QY 121 AMYTCARADNYFDIVGTYSHYFDYWGRTLVTVSS 156
DB 111 AVYTCARSHYVG-----SYDEFYWGQGTTLTVSS 140
RESULT 8
HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -/- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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CC -----
DR EMBL; J00494; AAA38130.1; -
DR PIR; A02042; HVMSB1.
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Query Match 48.0%; Score 402; DB 1; Length 117;

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RESULT 11
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region 102 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX STRAIN=C57BL/6;
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02032; HVM502.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 47.3%; Score 396; DB 1; Length 117;
Best Local Similarity 60.3%; Pred. No. 6.8e-32;
Matches 76; Conservative 17; Mismatches 23; Indels 10; Gaps 1;

QY 1 MDWTRILFLVAATGAHSOVQLVQSGAEVKPGASVKYCKSGYNFTGYSGASGHIFTA 60
DB 1 MGWSCIILFLVATATGVSHVQLQPGAEVLKPGASVKSCASGYT-----FTS 50

QY 61 YSVHWVRQAPQGLWGRNPNNSGATDYAHKFGQRTVMSRDTISITAYMELSLRLTSDDT 120
DB 51 YWHEWVKRQPGQGLWGRNPNNSGATDYAHKFGQRTVMSRDTISITAYMELSLRLTSDDT 110

QY 121 AMYICA 126
DB 111 AVYICA 116

RESULT 12
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region VH58 B4 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX STRAIN=C57BL/6;
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02032; HVM502.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 45.5%; Score 381; DB 1; Length 117;
Best Local Similarity 56.7%; Pred. No. 2e-30;
Matches 72; Conservative 18; Mismatches 27; Indels 10; Gaps 1;

QY 1 MDWTRILFLVAATGAHSOVQLVQSGAEVKPGASVKYCKSGYNFTGYSGASGHIFTA 60
DB 1 MGWSCIILFLVATATGVSHVQLQPGAEVLKPGASVKSCASGYT-----FTS 50

QY 61 YSVHWVRQAPQGLWGRNPNNSGATDYAHKFGQRTVMSRDTISITAYMELSLRLTSDDT 120
DB 51 YWHEWVKRQPGQGLWGRNPNNSGATDYAHKFGQRTVMSRDTISITAYMELSLRLTSDDT 110

QY 121 AMYICAR 127
DB 111 AVYICTR 117

RESULT 13
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX STRAIN=C57BL/6;
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
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RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL; J00533; AAA38602.1; -.
DR PIR; C90809; HVMS45.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 45.4%; Score 380; DB 1; Length 117;
Best Local Similarity 57.5%; Pred. No. 2.5e-30;
Matches 73; Conservative 18; Mismatches 26; Indels 10; Gaps 1;

QY 1 MDWTWILFLVAATGAHQVQLVQSGAEVKPGASVKVCKTSGYNFTGYSASGHIFTA 60
DB 1 MGWSCIIMFLAATATCVHFQVQLQPGALVLPKGVSKLSSKASGYT-----FTS 50

QY 61 YSVHWYRQAPGQLEWNGINPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSRITSD 120
DB 51 YNHWYKQRPGRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSLTSDS 110

QY 121 AMYICAR 127
DB 111 AVYICAR 117

RESULT 14
HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Szekevitcz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production; the dominant anti-arsonate
RL idiootype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
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CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; IMCP.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; PF04E4A167B654AF CRC64;

Query Match 45.4%; Score 380; DB 1; Length 120;
Best Local Similarity 53.7%; Pred. No. 2.6e-30;
Matches 73; Conservative 23; Mismatches 24; Indels 16; Gaps 2;

QY 21 VQLVQSGAEVKPGASVKVCKTSGYNFTGYSASGHIFTAYSVHWYRQAPGQLEWNGRI 80
DB 1 VQLVQSGAEVLVRAGSSVMSCKASGYT-----FTSYGINWVKRPGQGLEWIGYI 50

QY 81 NPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSRITSDDTAMYYCARADNYFDIVTGYTS 140
DB 51 NPGNGYTKYNEKFKGKTLTVDKSSSTAYMQLSLTSDSASVYFCARSVYVG-----S 104

QY 141 HYPDYWGRCGLTVTVSS 156
DB 105 YYPDYQGQGTTLTVSS 120

RESULT 15
HV50 MOUSE STANDARD; PRT; 120 AA.
ID HV50 MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RA "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 44.6%; Score 373.5; DB 1; Length 120;
Best Local Similarity 53.3%; Pred. No. 1.1e-29;
Matches 73; Conservative 18; Mismatches 29; Indels 17; Gaps 2;

QY 20 VQLVQSGAEVKPGASVKVCKTSGYNFTGYSASGHIFTAYSVHWYRQAPGQLEWNGR 79
DB 1 VQLVQSGAEVLVRAGSSVMSCKASGYT-----FTSYWVWVIRPGQGLEWIGG 50

QY 80 INPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSRITSDDTAMYYCARADNYFDIVTGYT 139
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Search completed: April 5, 2004, 13:24:55
Job time : 7.1269 secs


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QY 121 AMYCARADNYFDIVTGYTSHYFDYNGRGLTVTSS 156
DB 111 AIYFCARGNLGRGFGY--NWDPWGHGLTVTSS 144

RESULT 2
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AA09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
DR PROSITE; PS00835; Ig LIKE; 5.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 60.7%; Score 508; DB 4; Length 614;
Best Local Similarity 65.0%; Pred. No. 8.1e-42;
Matches 104; Conservative 15; Mismatches 17; Indels 24; Gaps 4;

QY 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
QY 61 YS-VHVVWRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSD 119
DB 50 YRLVHVVWRQAPGQALEWNGWITFPNGNTNVAQFQDRVITDRSMTAYMELSLRSED 109
QY 120 TAMYCARADNYFDIVTGYTSHY----FDYNGRGLTVTSS 156
DB 110 TAMYCAR-----GYSSWDADFQWQGTMTVTSS 140

RESULT 3
Q9ERV0 PRELIMINARY; PRT; 500 AA.
AC Q9ERV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Prostate;
RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AA05951.1; -.
DR HSPF; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; Ig LIKE; 4.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BFA43F2A3CC6D9 CRC64;

Query Match 60.2%; Score 503.5; DB 4; Length 500;
Best Local Similarity 65.0%; Pred. No. 1.7e-41;
Matches 102; Conservative 11; Mismatches 33; Indels 11; Gaps 2;

QY 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAATGAHSQVLVQSGAEVKKPGASVKYSCKTSGY-----AFHT 50
QY 61 YSVHVVWRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSD 120
DB 51 YSLVHVVWRQAPGQGLEWNGWISPSNDNTRFAKFKQGRVLTITDTSTVYMEALSRLSD 110
QY 121 AMYCARA-DNYFDIVTGYTSHYFDYNGRGLTVTSS 156
DB 111 AVYCARRYCSYSSQNDYYYYNDYMDVWGKGTITVTSS 147

RESULT 4
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5
DT 01-CCT-2003 (TrEMBLrel. 25, Created)
DT 01-CCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Rana S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettaman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Schmutz J.; Smallus D.E.; Schnerch A.; Schein J.B.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AA051328.1; -.
KW Hypothetical protein.
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SQ SEQUENCE 469 AA; 51395 MW; C8D5B21BAAF795C CRC64;
Query Match 59.0%; Score 493.5; DB 4; Length 469;
Best Local Similarity 64.1%; Pred. No. 1.6e-40;
Matches 100; Conservative 13; Mismatches 26; Indels 17; Gaps 3;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKFGASVKVSKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIFLVAAATGARQPVLHVQSGAEVKKFGASVLLSKTSGYN-----FSS 50
QY 61 YSVHWVROAPQGQLEWGRINPNSGATDYAHKFGQVMTSDTSTAYMELSLRLTSDDT 120
DB 51 YDIWVROAPQGQLEWGRINPNSGATDYAHKFGQVMTSDTSTAYMELSLRLTSDDT 110
QY 121 AMYICARADNFYDVTGTYSHFYDYGRTGLTVSS 156
DB 111 ALFYCATKSR-----GQVGD-FDSWQGLTVTVSS 139
RESULT 5
ID Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Putative matrix cell adhesion molecule-3.
DE IGG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacquemin M.G., Vander Elst L.P.L.;
RT MEDLINE=98322155; PubMed=9657749;
RL "Mechanism and kinetics of factor VIII inactivation: study with an
IG19 monoclonal antibody derived from a hemophilia A patient with
inhibitor";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAAL1829.1; -.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;
Query Match 58.9%; Score 493; DB 4; Length 150;
Best Local Similarity 63.5%; Pred. No. 4e-41;
Matches 99; Conservative 10; Mismatches 27; Indels 20; Gaps 2;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKFGASVKVSKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIFLVAAATGTHAQVQLVQSGAEVKKFGASVKVSKSGYT-----LTE 50
QY 61 YSVHWVROAPQGQLEWGRINPNSGATDYAHKFGQVMTSDTSTAYMELSLRLTSDDT 120
DB 51 LPVHWVQAPGKLEWVGSFDPESGESIYAREFGVQSTWMTADTSTDIAYMELSLRLSDDT 110
QY 121 AMYICARADNFYDVTGTYSHFYDYGRTGLTVSS 156
DB 111 AVYICAVPD-----PDADFQWGGTMTVTSS 136
RESULT 6
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Q96QSO
ID Q96QSO PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Putative matrix cell adhesion molecule-3.
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV039025; AAK82649.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;
Query Match 58.5%; Score 489.5; DB 4; Length 159;
Best Local Similarity 60.4%; Pred. No. 9.5e-41;
Matches 96; Conservative 17; Mismatches 33; Indels 13; Gaps 2;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKFGASVKVSKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKFGASVKVSKASGYTFSN-----50
QY 61 YSVHWVROAPQGQLEWGRINPNSGATDYAHKFGQVMTSDTSTAYMELSLRLTSDDT 120
DB 51 YTMWVROAPQGQPEWGMVNPSPGSGARSYQKQFQRLTMDTSTVTMDLSLRSDDT 110
QY 121 AMYICARADNFY---DIVTGYTSHFYDYGRTGLTVSS 156
DB 111 AVYICAREWEIFFGAVSKGFFYYGMDVWGGTMTVTSS 149
RESULT 7
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Putative matrix cell adhesion molecule-3.
DE Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 119 119
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345F4A16E CRC64;
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	Query Match	56.9%; Score 476; DB 4; Length 119;
	Best Local Similarity	69.3%; Pred. No. 1.4e-39;
	Matches	95; Conservative 10; Mismatches 14; Indels 18; Gaps 2;
QY	20 QVQLVQSGLAVKKPGASVKVSCKTSYGNYFTGYSASGHIFTAYSVHHVROAPQGGLWNGR	79
Db	1 EQVLVESGAELVKKPGASVKVSCKASGYTFTG-----YYMHVROAPQGGLWNGM	50
QY	80 INPNSGATDYAHKFGQRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNFDIVTGVT	139
Db	51 INPNSHTTYNAQKFQGVKTMTKDTSISTAYMELSRLSDDTAIYYCARG-----GGR	102
QY	140 SHYFDYWGRGTLTVTVSS 156	
Db	103 GLWFDPWGQGTILTVTVSS 119	
RESULT 8		
Q9UL95	PRELIMINARY; PRT; 125 AA.	
ID	Q9UL95 PRELIMINARY; PRT; 125 AA.	
AC	Q9UL95;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=36271739; PubMed=9614934;	
RA	Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M., Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetuses";	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
DR	EMBL; AF035019; AAD56255.1; --	
DR	HSP; P01810; 2FBJ.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig_1.	
DR	SMART; SMC0406; IGv; 1.	
DR	PROSITE; PS50835; IG_LIKE; 1.	
FT	NON_TER 125 125	
FT	NON_TER 125 125	
SQ	SEQUENCE 125 AA; 13516 MW; OD3CDSC232488EAC CRC64;	
Query Match	56.9%; Score 476; DB 4; Length 125;	
Best Local Similarity	69.3%; Pred. No. 1.5e-39;	
Matches	95; Conservative 10; Mismatches 20; Indels 12; Gaps 2;	
QY	20 QVQLVQSGLAVKKPGASVKVSCKTSYGNYFTGYSASGHIFTAYSVHHVROAPQGGLWNGR	79
Db	1 EQVLVESGAELVKKPGASVKVSCKASGYTFTG-----YYMHVROAPQGGLWNGM	50
QY	80 INPNSGATDYAHKFGQRVTMSRDTSISTAYMELSRLTSDDTAMYYCARADNFDIVTGVT	139
Db	51 INPNSGNTTYNAQKVQGRVTMTDITISITAYMELSRLSDDTAIYYCARGSGGRIAA--A	108
QY	140 SHYFDYWGRGTLTVTVSS 156	
Db	109 GDAFDIWGQGTMTVTVSS 125	
RESULT 9		
O95978	PRELIMINARY; PRT; 157 AA.	
ID	O95978 PRELIMINARY; PRT; 157 AA.	
AC	O95978;	
DT	01-MAY-1999 (TrEMBLrel. 10, Created)	
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	

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DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypochemical protein.
SQ SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;

Query Match
Best Local Similarity 55.7%; Score 466.5; DB 4; Length 496;
Matches 93; Conservative 18; Mismatches 31; Indels 15; Gaps 3;

QY 1 MDWTRILFLVAAATGAHSCVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTRILFLVAAATGAHSCVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLVWNGRINPNSGATDYAHKFGQVRVMSRDTISITAYMELSRITSDT 120
DB 51 YAFWTRVQAPGQGLWNGGIIFNFGAPNVAQNFQDRVITISADSTTTVMELTSLTFEDT 110
QY 121 AMYICARADNYFDIVTGYTSHYF-DYWGRTGLTVVSS 156
DB 111 AFYICGRGLTY-----GSGSYLQHWGQGLTVTVSS 143

RESULT 11
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment)
DE Homo sapiens (Human)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.B., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RA fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL; AF035022; AAD56258.1; -.
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match
Best Local Similarity 54.9%; Score 459.5; DB 4; Length 124;
Matches 91; Conservative 12; Mismatches 21; Indels 13; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQGLWNGR 79
DB 1 EVQLVDSGAEVKKPGASVKVSCKASGYT-----FSSYTHWVRQAPGQGLWNGI 50
QY 80 INFNSGATDYAHKFGQVRVMSRDTISITAYMELSRITSDTAMYYICARADNYFDIVTGYT 139
DB 51 INFSGGSTSYAQKFGQVRVMTTRDTSTVTMELSLRSDSTAVYYCARG--LYVVVPA 107
QY 140 SHYFDYWGRTGLTVVSS 156
DB 108 FSRFDYWGQGLTVVSS 124

Query Match
Best Local Similarity 54.7%; Score 458; DB 11; Length 473;
Matches 85; Conservative 25; Mismatches 28; Indels 18; Gaps 2;

QY 1 MDWTRILFLVAAATGAHSCVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 NEWSVFLFLISVTAGVHCQVQLKQSGAEVKKPGASVKISCKASGYTFD-----50
QY 61 YSVHWVRQAPGQGLVWNGRINPNSGATDYAHKFGQVRVMSRDTISITAYMELSRITSDT 120
DB 51 YYINWVRQPGQGLWIGTKIPGSGSTYYNEKFKGATLTADKSSSTAYVQLSLTSEDS 110
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTGLTVVSS 156
DB 111 AVYFCAR-----SGDYDWFAYWGQGLTVTVSA 138

RESULT 13
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

```


This sequence represents the heavy chain variable region of the monoclonal antibody (MAB), KR1X1. This MAB produced by the cell line of the invention, specifically recognises the wild type factor VIII light chain. KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand factor in a dose dependant manner. The new cell line KR1X1, is deposited with the Belgian Coordinated Collections of Micro-organisms, under accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with a thrombolytic agent, are useful for the treatment and/or prevention of hemostasis, coagulation disorder or thrombotic pathologic condition such as intravascular coagulation, arterial thrombosis, arterial restenosis, venous thrombosis or arteriosclerosis, and attenuation of coagulation in a mammal. An effective and safe antithrombotic therapy is provided which reduces the risk of bleeding in mammals, more particularly in humans

XX SQ Sequence 156 AA;

Query Match 100.0%; Score 837; DB 4; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3.7e-71; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0;
 QY 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
 DB 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60
 QY 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 120
 DB 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 120
 QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
 DB 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

RESULT 2

AAO18878
 ID AAO18878 standard; protein; 156 AA.

XX AC AAO18878;

DT 07-NOV-2002 (first entry)

DE Human KR1X1 heavy chain variable region.

XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation; variable region; factor VIII inhibitor; sepsis; septic shock; thrombus formation; systemic inflammatory response syndrome; CDR; disseminated intravascular coagulation; haemophilia A; immunosuppressive; complementarity determining region; antibacterial; antiinflammatory.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 42..64 /label= CDR1
 FT Region 79..95 /label= CDR2
 FT Region 128..145 /label= CDR3

XX EP1222929-A2.

XX PD 17-JUL-2002.

XX PF 11-JAN-2002; 2002EP-00447005.

XX PR 11-JAN-2001; 2001US-0261405P.

XX PA (COLL-) COLLEN RES FOUND VZW D.

XX PI Jacquemin MG, Saint-Remy JR;

XX DR WPI; 2002-610270/66.

DR N-PSDB; AAL49256.

XX Pharmaceutical composition for treating systemic inflammatory response syndrome, sepsis, septic shock and/or thrombus formation in microvasculature in mammals, comprises a partial inhibitor of factor VIII.

XX PS Disclosure; Fig 12; 41pp; English.

XX The present invention relates to a pharmaceutical composition for the prevention and/or treatment of systemic inflammatory response syndrome (SIRS), sepsis, septic shock, thrombus formation in the microvasculature and disseminated intravascular coagulation in mammals, comprising as an active ingredient a partial inhibitor of factor VIII, in admixture with a carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The present sequence is the heavy chain variable region of KR1X1

XX SQ Sequence 156 AA;

Query Match 100.0%; Score 837; DB 5; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3.7e-71; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0;

QY 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60

DB 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKYSCKTSGYNFTGYSASGHIFTA 60

QY 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 120

DB 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 120

QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

DB 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

RESULT 3

ADE28427
 ID ADE28427 standard; protein; 471 AA.

XX AC ADE28427;

DT 29-JAN-2004 (first entry)

XX Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.

DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; variable region heavy chain; 21-2-1.

XX OS Homo sapiens.

XX PN WO2003040170-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-US036107.

XX PR 09-NOV-2001; 2001US-0346980P.

XX PA (PFIZ) PFIZER PROD INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX DR WPI; 2003-441521/41.

XX DR N-PSDB; ADE28426.

XX New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.

XX Claim 1; SEQ ID NO 34; 177pp; English.

PS The invention relates to a novel chimeric or human monoclonal antibody or

XX its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40

CC antibody variable region heavy chain protein of the invention.

XX

SQ Sequence 471 AA;

Query Match 73.1%; Score 611.5; DB 7; Length 471;

Best Local Similarity 76.9%; Pred. No. 2.8e-49;

Matches 120; Conservative 7; Mismatches 18; Indels 11; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 120

Db 51 YYNHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 110

QY 121 AMYTCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

Db 111 AVYTCAR-DQPLGCTNGVCSYFDYWGQGLTVTVSS 145

RESULT 4

AAU74296

ID AAU74296 standard; protein; 470 AA.

XX AAU74296;

AC

DT 12-MAR-2002 (first entry)

DE

XX Anti-human AILIM monoclonal antibody clone Jmab-136, heavy chain.

XX Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotrophic;

KW immunosuppressive; dermatological; antiinflammatory; hepatotopic;

KW activation inducible lymphocyte immunomodulatory molecule; AILIM;

KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;

KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;

KW allergic contact-type dermatitis; chronic inflammatory dermatosis;

KW systemic lupus erythematosus; autoimmune disorder; inflammation;

KW graft versus host reaction; immune rejection; intestinal immunity;

KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

XX

OS Homo sapiens.

XX

XX WO200167981-A2.

XX

XX 22-NOV-2001.

XX

XX 15-MAY-2001; 2001WO-JP004035.

XX

XX 18-MAY-2000; 2000JP-00147116.

PR 30-MAR-2001; 2001JP-00099508.

XX

XX (NISR) JAPAN TOBACCO INC.

XX

XX Tsuji T, Tezuka K, Hori N;

XX

XX WPI; 2002-075313/10.

DR N-PSDB; AAS99472.

XX

PT New human monoclonal antibody that binds to activation inducible

PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid

PT arthritis, multiple sclerosis and inflammation.

XX

XX Claim 30; Page 264-266; 300pp; English.

XX

XX The invention relates to a novel human antibody (I), preferably a human

CC monoclonal antibody which binds to an activation inducible lymphocyte

CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal

CC transduction into a cell mediated by AILIM, for modulating proliferation

CC of AILIM-expressing cells, for modulating production of a cytokine from

CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity

CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of

CC AILIM-expressing cells. (I) is useful for treating, preventing or

CC prophylaxis of delayed type allergy. (I) is useful for treating and

CC preventing various diseases associated with AILIM-mediated costimulatory

CC transduction, and for inhibiting the onset and/or advancement of the

CC diseases. (I) is useful for suppression, prevention and/or treatment of

CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,

CC allergic contact-type dermatitis, chronic inflammatory dermatosis,

CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,

CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus

CC host reaction, graft versus host disease, immune rejection, disorders

CC caused by abnormal intestinal immunity, specifically inflammatory

CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,

CC nephritis, vasculitis, and pancreatitis. (I) induces no serious

CC immunorejection due to antigenicity to human, i.e., human anti-mouse

CC immunorejection (HAMA) in a host. AAU74296-AAU74301 represent anti-human

CC AILIM monoclonal antibody amino acid sequences of the invention

XX

SQ Sequence 470 AA;

Query Match 72.5%; Score 607; DB 5; Length 470;

Best Local Similarity 76.3%; Pred. No. 7.5e-49;

Matches 119; Conservative 9; Mismatches 16; Indels 12; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60

Db 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 120

Db 51 YYNHWVRQAPGQGLEWMGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLTSDDT 110

QY 121 AMYTCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

Db 111 AVYTCAR--TYVDSGYTHDAFDINGQGTMTVTVSS 144

RESULT 5

AAW22841

ID AAW22841 standard; protein; 146 AA.

XX AAW22841;

AC

XX 12-SEP-1997 (first entry)

DT

XX Human anti-tumour antigen antibody heavy chain variable region.

DE

XX Human; tumour antigen; cancer; monoclonal; antibody; heavy chain;

KW variable region; medicine; pharmacology; biochemistry; CDR;

KW complementarity determining region.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

FF 1..19 /label= sig_peptide

FT Peptide

FT 20..146 /label= mat_peptide

FT Peptide

FT 50..54 /label= CDR_1

FT 69..85

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FT Region /label= CDR_2
FT 118..1139
FT /label= CDR_3
XX
PN JP09100300-A.
PD 15-APR-1997.
XX
PF 03-OCT-1995; 95JP-00278266.
XX
PR 03-OCT-1995; 95JP-00278266.
XX
PA (HAGI/) HAGIWARA Y.
XX
DR WPI; 1997-276726/25.
DR N-PSDB; AAT75422.
XX
PT Anticancer human monoclonal antibody variable region sequences - and
PT related DNA and RNA.
XX
PS Claim 3; Page 10; 14pp; Japanese.
XX
CC The present sequence is a human anti-tumour antigen monoclonal antibody
CC (Mab) heavy chain variable region, useful in medicine, pharmacology and
CC biochemistry. The isotype of a Mab secreted by the human/human hybridoma
CC HT was determined to be mu and kappa. Human Mab was purified, and the
CC antigen recognised by human Mab CLN"-IgM identified by western blotting
XX
XX Sequence 146 AA;
SQ
Query Match 70.0%; Score 586; DB 2; Length 146;
Best Local Similarity 72.8%; Pred. No. 1.8e-47;
Matches 118; Conservative 6; Mismatches 12; Indels 26; Gaps 4;
QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKFGASVKVCKTSYGNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKFGASVKVCKTSYGNFTGYSASGHIFTA 50
QY 61 YSVHWVQAPQGLEWGRINPNSGATDYAHKFGQVTRMSRDTISISTAYMELSLTSDDT 120
DB 51 YYHWVQAPQGLEWGRINPNSGGTNYAQKFGQVTRDTISISTAYMELSLRSDDT 110
QY 121 AMYTCARADNVFDIVTG---TGHYFDY-----WGRGTLV 152
DB 111 AVYTCARGPK-----GYCSTSCYFDYVYGGVMDVWGQGTTV 146
RESULT 6
AAB36215
XX AAB36215 standard; protein; 236 AA.
XX
XX AAB36215;
XX
DT 15-FEB-2001 (first entry)
XX
XX Human immune system associated protein HISAP-13.
XX
XX Human; immune system associated protein; HISAP-13; immune disorder;
XX infection; autoimmune disease; cancer.
XX
XX Homo sapiens.
XX
XX US6135941-A.
XX
XX 24-OCT-2000.
XX
XX 27-MAR-1998; 98US-00049672.
XX
XX 27-MAR-1998; 98US-00049672.
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;

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PI Hillman JL, Au-Young J;
XX
XX WPI; 2001-030926/04.
DR N-PSDB; AAC66531.
XX
XX New human immune system associated proteins (HISAP) and polynucleotides
XX encoding the HISAP, useful for diagnosing, treating or preventing immune
XX or cell proliferative disorders or infections.
XX
XX Claim 1; Col 71-72; 54pp; English.
XX
XX The present invention provides the coding and protein sequences for a
XX number of human immune system associated proteins (HISAPs). These can be
XX used in the diagnosis and treatment of various autoimmune disorders,
XX infections and cell proliferation diseases. The diseases include AIDS,
XX adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
XX Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
XX gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
XX erythematosus, arteriosclerosis, cirrhosis and cancer
XX
XX Sequence 236 AA;
SQ
Query Match 65.8%; Score 550.5; DB 4; Length 236;
Best Local Similarity 70.7%; Pred. No. 7.2e-44;
Matches 111; Conservative 13; Mismatches 14; Indels 19; Gaps 4;
QY 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKFGASVKVCKTSYGNFTGYSASGHIFTA 60
DB 1 MDWTWRLFLVAAATGAHSQVLVQSGAEVKKFGASVKVCKTSYGNFTGYSASGHIFTA 50
QY 61 YSVHWVQAPQGLEWGRINPNSGATDYAHKFGQVTRMSRDTISISTAYMELSLTSDDT 120
DB 51 YAMHWVQAPQGLEWGRINAGNNTKYSONFGQRTITRTDTSASTAYMELSLRSED 110
QY 121 AMYTCARADNVFDIVTG-YTSHFDYVGRGTLVTVSS 156
DB 111 AVYTCAR-----VWAGEFTS--FDYWGQGTTLVTVSS 139
RESULT 7
AAB6296
XX AAB6296 standard; protein; 117 AA.
XX
XX AAB6296;
XX
XX 25-MAR-2003 (revised)
XX
XX 07-AUG-1995 (first entry)
XX
XX Human immunoglobulin variable heavy chain #2.
XX
XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
XX cosmid; placenta; vector; pJB81; E.coli; mammalian.
XX
XX Homo sapiens.
XX
XX WO9426895-A1.
XX
XX 24-NOV-1994.
XX
XX 10-MAY-1993; 93WO-JP000603.
XX
XX 10-MAY-1993; 93WO-JP000603.
XX (NISB) JAPAN TOBACCO INC.
XX
XX Honjo T, Matsuda F;
XX
XX WPI; 1995-006791/01.
DR N-PSDB; AAQ78940.
XX
XX DNA fragment comprising human immunoglobulin Vh genes - for the
XX production of human immunoglobulin in mammalian hosts.
XX

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PS Disclosure; Page 32-33; 130pp; Japanese.

XX Protein sequences (AAR6295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; CC Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh CC genes. The fragments cover a region of 800 kb. The DNA fragments were CC isolated from high molecular weight DNA from human placenta. The DNA was CC partially digested with TaqI restriction enzyme. The fragments were CC separated by gel electrophoresis and 35-45 kb fractions were collected. CC The fragments were ligated with ClaI-digested cosmid vector pJB81. The CC ligation products were in vitro packed and infected into E.coli 490A. The CC fragments were then subcloned by colony hybridisation. The Vh genes and CC the DNA fragments encoding them are useful in producing human CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN CC field.)

XX SQ Sequence 117 AA;

Query Match 65.7%; Score 550; DB 2; Length 117;

Best Local Similarity 83.5%; Pred. No. 3.5e-44;

Matches 106; Conservative 4; Mismatches 7; Indels 10; Gaps 1;

QY 1 MDWTWRIELVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGSGYFTG----- 50

DB 1 MDWTWRIELVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGSGYFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 120

DB 51 YNHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 110

QY 121 AMYICAR 127

DB 111 AVYICAR 117

RESULT 8

AAAY96295

ID AAY96295 standard; protein; 148 AA.

AC AAY96295;

XX 16-AUG-2000 (first entry)

DE Human IGFAM-7 immunoglobulin.

XX Human; immunoglobulin; IGFAM-7; IGFAM; immune disorder; cancer;

KW infection; inflammation; haematopoiesis; AIDS; allergy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= signal_peptide

FT Protein 20..148

FT /label= IGFAM-7

FT Domain 34..117

FT /label= Ig_domain

XX WO200029583-A2.

PN 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

PI Lu D&M, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

DR N-PSDB; AA427367.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with PT altered levels of the protein such as cancer, immune system disorders.

XX Claim 1; Page 83; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein IGFAM-7. Its gene was isolated from a cDNA library of bladder tumour CC tissue. It is expressed in reproductive, gastrointestinal and immune and CC haematopoietic tissue, where cancer and inflammation are common. The CC gene, protein, its antibodies, agonists and antagonists are suitable for CC diagnosing and treating many diseases, including cancer, immune system CC disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, hepatitis, CC disease, diabetes mellitus, emphysema, Graves' disease, scleroderma, CC multiple sclerosis, psoriasis, rheumatoid arthritis, complications of CC cancer, haemodialysis and extracorporeal circulation, trauma and CC haematopoietic cancer (such as leukaemia) and infections caused by CC bacteria, viruses, fungi or parasites

XX SQ Sequence 148 AA;

Query Match 65.4%; Score 547.5; DB 3; Length 148;

Best Local Similarity 68.6%; Pred. No. 7.9e-44;

Matches 107; Conservative 11; Mismatches 19; Indels 19; Gaps 2;

QY 1 MDWTWRIELVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGSGYFTG----- 50

DB 1 MDWTWRIELVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKGSGYFTG----- 50

QY 61 YSVHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 120

DB 51 YNHWVRQAPGQGLEWMGRIINPNSGATDYAHKFQGRVTMSRDTSTAYMELSLRLTSDT 110

QY 121 AMYICARADNYFDIVTGYTSHYFDYVGRGLTVTVSS 156

DB 111 AIYYCARGD-----YGNSLDHWGQGNLTVTVSS 137

RESULT 9

ABP57367

ID ABP57367 standard; protein; 145 AA.

AC ABP57367;

XX 22-APR-2003 (first entry)

DE Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.

XX Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;

KW antibody therapy.

XX Homo sapiens.

XX Synthetic.

XX WO200294880-A1.

PN 28-NOV-2002.

XX 17-MAY-2002; 2002WO-JP004816.

XX 18-MAY-2001; 2001JP-00150213.

XX 09-AUG-2001; 2001JP-00243040.

XX 11-OCT-2001; 2001JP-00314489.

XX (KIRI) KIRIN BEER KK.

PI Mori E, Kataoka S;
 XX WPI; 2003-120790/11.
 DR N-PSDB; AB259698.
 XX
 XX New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
 PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
 PT nor inducing injury to hepatocytes, for use in therapy of malignant
 PT tumor.
 XX
 XX Claim 54; Page 62; 92pp; Japanese.
 PS
 XX The present invention describes antibodies or their functional fragments
 CC that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
 CC have cytostatic and apoptotic activities, and can be used in antibody
 CC therapy. The antibodies can be applied as remedies and preventives of
 CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
 CC in the therapy of malignant tumours. Remedies produced with the
 CC antibodies are highly safe, and avoid hepatotoxicity. The present
 CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
 CC present invention
 XX
 XX Sequence 145 AA;
 SQ
 Query Match 65.1%; Score 544.5; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 1.5e-43;
 Matches 109; Conservative 14; Mismatches 16; Indels 23; Gaps 3;
 QY 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
 DB 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKPGASVKVSCKTSGYFTN----- 50
 QY 61 YSVHVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRSDT 120
 DB 51 YKINWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRSDT 110
 QY 121 AMYICARADNYFDIVTGYTSHYFDY-----WGRGLTVTVSS 156
 DB 111 AVYICARS-----YGSQSYRDYTYGDMVWGQGTIVTVSS 145
 RESULT 10
 AAB53510
 ID AAB53510 standard; protein; 146 AA.
 XX
 AC AAB53510;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SEQ ID NO:1050.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; anti-infective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200005351-A1.
 XX
 XX 21-SEP-2000.
 PD
 XX 08-MAR-2000; 2000WO-US005883.
 PF
 XX 12-MAR-1999; 99US-0124270P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM;
 PI
 XX

DR WPI; 2000-587534/55.
 DR N-PSDB; AAC98267.
 XX
 XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.
 XX
 XX Claim 11; Page 1631; 2104pp; English.
 PS
 XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, anti-infective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention
 XX
 XX Sequence 146 AA;
 SQ
 Query Match 64.6%; Score 540.5; DB 3; Length 146;
 Best Local Similarity 67.5%; Pred. No. 3.6e-43;
 Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;
 QY 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
 DB 6 MDWTRILFLVAAATGAHSQVQLVQSGAEVKPGASVKVSCKASGYT-----FTS 55
 QY 61 YSVHVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRSDT 120
 DB 56 YDINWVRQATGQGLEWMGRINPNSANTGYAOKFGQRTVMSRDTISITAYMELSLRSDT 115
 QY 121 AMYICARADNY-----FDIVTGYTSHYFDYWGRTVTV 154
 DB 116 AVYICARXRRLGLGMWD-----FDYWGQGTIVTV 146
 RESULT 11
 AAB88464
 ID AAB88464 standard; protein; 476 AA.
 XX
 AC AAB88464;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 XX Monoclonal antibody 4B5 heavy chain variable region.
 DE
 XX Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
 XX diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
 KW lung carcinoma; metastasis; anti-idiotypic antibody; GD2 antigen; human.
 KW
 XX Homo sapiens.
 OS
 XX WO9902545-A2.
 XX
 XX 21-JAN-1999.
 PD
 XX 08-JUL-1998; 98WO-IB001046.
 PF
 XX 08-JUL-1997; 97US-0051945P.
 PR
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 PA
 XX Dan MD;
 PI
 XX WPI; 1999-120769/10.
 DR

DR N-PSDB; AAX06951.
XX New antibody 4B5 polynucleotides and polypeptides - used to develop
PT products for the diagnosis and treatment of cancers and for prophylactic
PT therapy to reduce risk of recurrence.
XX
XX
XX Claim 1; Page 79-80; 83pp; English.
XX
XX This polypeptide comprises the heavy chain variable region of the
CC recombinant human monoclonal antibody (MAB), 4B5. 4B5 recognises
CC antibodies specific for GD2 antigen antibodies. Antibodies specific for
CC GD2 recognise various cancers including glioblastoma, neuroblastoma,
CC malignant and/or metastatic melanoma, breast adenocarcinoma, lung
CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
CC immunologic specificity for antibodies specific for GD2. These
CC derivatives, or antigen binding fragments, comprise regions of the 4B5
CC VDJ junction and regions spanning the 4B5 CDRs. Other derivatives include
CC Fab, F(ab')₂, Fab', scFv and isolated heavy and light chains (see also
CC AAX06951). Polynucleotide fragments (see AAX06951-54) encoding 4B5
CC antibody V regions are also provided, and therapeutic plasmids and
CC vectors, including vaccinia virus vectors, comprising these
CC polynucleotides. 4B5 has been shown to mimic GD2, and is particularly
CC useful in generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g. astrocytoma,
CC oligodendroglioma, ependymoma, medulloblastoma, primitive neural
CC ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
CC large cell lung adenocarcinomas, squamous cell carcinoma,
CC bronchoalveolar carcinoma, epithelial adenocarcinoma, and liver metastases,
CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
CC adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
CC uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
CC transitional squamous cell carcinoma of the bladder, B and T cell
CC lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma
XX
XX Sequence 476 AA;
SQ
Query Match 64.5%; Score 540; DB 2; Length 476;
Best Local Similarity 68.6%; Pred. No. 1.6e-42;
Matches 109; Conservative 14; Mismatches 20; Indels 16; Gaps 4;
QY 1 MDWTWRLFLVAAATGASHQVQLVQSGAEVKPGASVKCKSTGYNFTGYSASGHFTFA 60
DB 1 MDWTWRLFLVAAATGASHQVQLVQSGAEVKPGASVKCKSTGYNFTGYSASGHFTFA 60
QY 61 YSVHWRQAPQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSRLTSDPT 120
DB 51 FDLNWRVQAPQGLEWMGRINPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSRLTSDPT 110
QY 121 AMYYCAR-ADNYFDIVTGYTSHYP--DYWGRGTLTVSS 156
DB 111 AVYFCARNADN---VENAAIYHYGYMDVWGQGTITVSS 146
RESULT 12
ABP45711
ID ASP45711 standard; protein; 250 AA.
XX
AC ABP45711;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1722.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS

XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-027379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2457-2458; 3149pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
SQ
Sequence 250 AA;
Query Match 64.4%; Score 539; DB 5; Length 250;
Best Local Similarity 75.9%; Pred. No. 9.4e-43;
Matches 104; Conservative 10; Mismatches 13; Indels 10; Gaps 1;
QY 20 QVQLVQSGAEVKPGASVKCKSTGYNFTGYSASGHFTAYSVHWRQAPQGLEWMGR 79
DB 1 QVQLVQSGAEVKPGASVKCKSTGYNFTGYSASGHFTAYSVHWRQAPQGLEWMGR 79
QY 80 INPNSGATDYAHKFGQGRVTMSRDTSTSTAYMELSRLTSDTAMYYCARADNYFDIVTGYT 139
DB 51 INPNSGGTNYAQKFGQGRVTMTSDTSTSTAYMELSRLTSDTAVYYCARVLPYDILTGY 110
QY 140 SHYEDYNGRGTLTVSS 156
DB 111 QNWFDPWGRGLTVSS 127
RESULT 13
AAV24370
ID AAV24370 standard; protein; 149 AA.
XX
XX AAV24370;
XX
XX 17-SEP-1999 (first entry)
XX
XX Human monoclonal antibody against CtGF SEQ ID NO:8.
XX
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
XX

KW cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
KW skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
XX rheumatic vascular inflammation.
OS Homo sapiens.
XX WO9933878-A1.
XX PD 08-JUL-1999.
XX PF 16-DEC-1998; 98WO-JP005697.
XX PR 25-DEC-1997; 97JP-00367699.
XX PR 13-DEC-1998; 98JP-00356183.
XX PA (NISR) JAPAN TOBACCO INC.
XX XX Tamatani T, Tezuka K, Sakamoto S, Takigawa M;
XX WPI; 1999-430232/36.
XX DR N-PSDB; AAX90021.
XX XX New monoclonal antibody reactive with connective tissue growth factor
PT useful in the treatment of cell proliferation disorders.
XX PS Claim 17; Page 177-178; 212pp; Japanese.
XX XX AAX90020 to AAX90029 encode monoclonal antibodies which react with human
CC connective tissue growth factor (CTGF). AAX24369 to AAX24378 represent
CC these monoclonal antibodies. The antibodies are useful in the diagnosis,
CC prevention and treatment of cell proliferation disorders in which CTGF is
CC implicated, including fibrosis of lung, kidney, liver and other tissues;
CC liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid arthritis;
CC rheumatic vascular inflammation; hepatitis; and cancer
XX SQ Sequence 149 AA;
Query Match 63.6%; Score 532; DB 2; Length 149;
Best Local Similarity 68.6%; Pred. No. 2.3e-42;
Matches 107; Conservative 9; Mismatches 26; Indels 14; Gaps 2;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKAFWL-----HLSPG 51
QY 61 YSVHWVRAQPGQGLEWNGRINPNSGATDYAHKFGQVMTMSRDTISITAYWELSLRLSDDT 120
Db 52 YNHWVRAQPGQGLEWNGRINPNSGTHYAQMFGQVTVTRDTISITAYWELSLRLSDDT 111
QY 121 AMYYCARADNYFDIVGTSHYFDYWGRTLVTVSS 156
Db 112 AVYYCAR-----EGIAAAAIYGMVWGQGTTLTVSS 142
RESULT 14
AAU31804
ID AAU31804 standard; protein; 746 AA.
XX AC AAU31804;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #2295.
XX KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX XX WO200179449-A2.
XX PN 25-OCT-2001.
XX PD

XX 16-APR-2001; 2001WO-US008656.
XX PR 18-APR-2000; 2000US-00552929.
XX PR 26-JAN-2001; 2001US-00770160.
XX XX (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX DR Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX PS Claim 20; Page 511; 765pp; English.
XX XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation, to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX SQ Sequence 746 AA;
Query Match 63.3%; Score 529.5; DB 4; Length 746;
Best Local Similarity 68.8%; Pred. No. 2.8e-41;
Matches 108; Conservative 9; Mismatches 23; Indels 17; Gaps 3;
QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
Db 5 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFNNGLA----- 58
QY 61 YSVHWVRAQPGQGLEWNGRINPNSGATDYAHKFGQVMTMSRDTISITAYWELSLRLSDDT 120
Db 59 -----WVRAQPGQGLEWNGWTIANGKTNIAQKQGRVTTTDTISTAYWELSLRLSDDT 114
QY 121 AMYYCARADNYFDIVGTSHYFDYWGRTLVTVSS 156
Db 115 AVYYCAREKDN-----ATGAWFAYWGQGTTLTVSS 145
RESULT 15
AAU80290
ID AAU80290 standard; peptide; 135 AA.
XX AC AAU80290;
XX DT 30-MAY-2000 (first entry)
XX DE Humanised anti-Fas antibody heavy chain variable region SEQ ID NO:10.
XX KW Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
KW diagnosis; CDR; complementarity determining region; apoptosis;
XX immunosuppressive.
XX OS Homo sapiens.
XX OS Mus sp.
XX PN JP2000014383-A.
XX PN

PD 18-JAN-2000.
XX
XX PF 03-JUL-1998; 98JP-00204318.
XX
XX PR 03-JUL-1998; 98JP-00204318.
XX
XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
XX DR WPI; 2000-199626/19.
XX
XX PT Novel recombinant antibody used for treating and diagnosing autoimmune
PT diseases - is humanized anti-Fas antibody which controls and induces
PT apoptosis in cells expressing fas antigen.
XX
XX PS Claim 13; Page 13; 25pp; Japanese.
XX
XX CC The present invention describes a recombinant antibody (A) which binds to
CC fas antigen, and controls and induces apoptosis in cells which expressed
CC fas antigen. The complementarity determining regions (CDR) of (A) contain
CC amino acid sequences obtained from a mammal other than human, other
CC regions contain amino acid sequences from human and they partly contain
CC modified amino acids. (A) has immunosuppressive activity. (A) is used for
CC treating and/or diagnosing autoimmune diseases. The present sequence
CC represents a specifically claimed heavy chain variable region of (A)
XX
SQ Sequence 135 AA;

Query Match 63.1%; Score 528.5; DB 3; Length 135;
Best Local Similarity 66.9%; Pred. No. 4.4e-42;
Matches 105; Conservative 12; Mismatches 17; Indels 23; Gaps 3;

QY 1 MDWTWRIILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSGYNFTGYSASGHIFTA 60
DB 1 MDWTWRIILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKASGYTFD----- 50

QY 61 YSVHWVROAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYWEISRLTSDDT 120
DB 51 YNHWVROAPGQGLEWIGYIYPYNGGTGYNQKPKATSTRDISITAYWEISRLTSEDS 110

QY 121 AMYYCARADNYFDIVTGYTSHY-FDYWGRGTLTVSS 156
DB 111 AMYYCAR-----SYAMDYWGQGTITVTVSS 135

Search completed: April 5, 2004, 13:24:17
Job time : 51.4162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: April 5, 2004, 13:42:12 ; Search time 36.6904 Seconds
(without alignments)
1116.513 Million cell updates/sec
Title: US-10-044-569B-6
Perfect score: 837
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1071436 seqs, 262597696 residues
Total number of hits satisfying chosen parameters: 1071436
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
Result No.	Score	Match	Length	DB	ID		
1	837	100.0	156	14	US-10-044-569B-6	Sequence 6, Appli	
2	607	72.5	470	9	US-09-859-053-28	Sequence 28, Appl	
3	540.5	64.6	146	9	US-09-925-299-1050	Sequence 1050, Ap	
4	540.5	64.6	146	10	US-09-925-299-1050	Sequence 1050, Ap	
5	540	64.5	476	9	US-09-747-669-3	Sequence 3, Appli	
6	540	64.5	476	14	US-10-290-703-3	Sequence 3, Appli	
7	539	64.4	250	10	US-09-880-748-1722	Sequence 1722, Ap	
8	532	63.6	149	14	US-10-390-986-8	Sequence 8, Appli	
9	527	63.0	250	10	US-09-880-748-1723	Sequence 1723, Ap	
10	525.5	62.8	146	14	US-10-390-986-12	Sequence 12, Appl	
11	525.5	62.8	256	10	US-09-880-748-1640	Sequence 1640, Ap	
12	523.5	62.5	139	10	US-09-269-921-123	Sequence 123, Appl	
13	523.5	62.5	139	10	US-09-509-098-45	Sequence 45, Appl	
14	523.5	62.5	139	14	US-10-218-253-123	Sequence 123, Appl	
15	523.5	62.5	146	14	US-10-390-986-10	Sequence 10, Appl	

16	522.5	62.4	432	12	US-10-389-223A-10	Sequence 10, Appl
17	522.5	62.4	480	12	US-10-389-223A-4	Sequence 4, Appl
18	522.5	62.4	601	12	US-10-380-438-3	Sequence 3, Appl
19	522.5	62.4	614	12	US-10-389-223A-2	Sequence 2, Appl
20	522.5	62.4	658	12	US-10-380-438-1	Sequence 1, Appl
21	520.5	62.2	197	15	US-10-264-049-4263	Sequence 4263, Ap
22	520.5	62.2	249	10	US-09-880-748-1635	Sequence 1635, Ap
23	519.5	62.1	139	10	US-09-269-921-108	Sequence 108, App
24	519.5	62.1	139	10	US-09-269-921-115	Sequence 115, App
25	519.5	62.1	139	10	US-09-509-098-16	Sequence 16, Appl
26	519.5	62.1	139	10	US-09-509-098-30	Sequence 30, Appl
27	519.5	62.1	139	14	US-10-218-253-108	Sequence 108, App
28	519.5	62.1	139	14	US-10-218-253-115	Sequence 115, App
29	518.5	61.9	139	10	US-09-269-921-124	Sequence 124, App
30	518.5	61.9	139	10	US-09-509-098-48	Sequence 48, Appl
31	518.5	61.9	139	14	US-10-218-253-124	Sequence 124, App
32	518.5	61.9	247	10	US-09-880-748-1729	Sequence 1729, App
33	517.5	61.8	139	9	US-09-760-723-7	Sequence 7, Appl
34	517.5	61.8	139	9	US-09-355-925-7	Sequence 7, Appl
35	517.5	61.8	139	10	US-09-269-921-121	Sequence 121, App
36	517.5	61.8	139	10	US-09-269-921-125	Sequence 125, App
37	517.5	61.8	139	10	US-09-509-098-42	Sequence 42, Appl
38	517.5	61.8	139	10	US-09-509-098-50	Sequence 50, Appl
39	517.5	61.8	139	14	US-10-315-125-7	Sequence 7, Appl
40	517.5	61.8	139	14	US-10-218-253-121	Sequence 121, App
41	517.5	61.8	139	14	US-10-218-253-125	Sequence 125, App
42	517.5	61.8	139	14	US-10-428-085-7	Sequence 7, Appl
43	516.5	61.7	139	10	US-09-269-921-109	Sequence 109, App
44	516.5	61.7	139	10	US-09-269-921-118	Sequence 118, App
45	516.5	61.7	139	10	US-09-509-098-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-044-569B-6
; Sequence 6, Application US/10044569B
; Publication No. US20030175269A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT FILING DATE: 2002-01-11
; CURRENT FILING DATE: 2002-01-11
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (124)..(192)
; OTHER INFORMATION: complementary determining region number one
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (232)..(285)
; OTHER INFORMATION: complementary determining region number two
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (282)..(435)
; OTHER INFORMATION: complementary determining region number three
; OTHER INFORMATION: complementary determining region number three
US-10-044-569B-6

Query Match 100.0%; Score 837; DB 14; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156

RESULT 2
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Teruka, Katsumari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match 72.5%; Score 607; DB 9; Length 470;
Best Local Similarity 76.3%; Pred. No. 7.8e-52;
Matches 119; Conservative 9; Mismatches 16; Indels 12; Gaps 2;

QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 51 YVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 110
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
Db 111 AVYICAR--TYVYDSSGYHDAFDINGQGTMTVTVSS 144

RESULT 3
US-09-925-299-1050
; Sequence 1050, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 1050
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1050

Query Match 64.6%; Score 540.5; DB 10; Length 146;
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 6 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 56 YDINWVRQATGQGLEWVGRINPNSANTGYAQKFGRTVTRNTSISTAYMELSLRLTSDDT 115
QY 121 AMYICARADNY-----FDIVTGYTSHYFDYWGRTLVTV 154
Db 116 AVYICARRRRWELLGWMWD-----FDYWGQGLIVTV 146

RESULT 5
US-09-747-669-3
; Sequence 3, Application US/09747669
```

```
; SEQ ID NO 1050
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1050

Query Match 64.6%; Score 540.5; DB 9; Length 146;
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 6 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 56 YDINWVRQATGQGLEWVGRINPNSANTGYAQKFGRTVTRNTSISTAYMELSLRLTSDDT 115
QY 121 AMYICARADNY-----FDIVTGYTSHYFDYWGRTLVTV 154
Db 116 AVYICARRRRWELLGWMWD-----FDYWGQGLIVTV 146

RESULT 4
US-09-925-299-1050
; Sequence 1050, Application US/09925299
; Patent No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1050
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1050

Query Match 64.6%; Score 540.5; DB 10; Length 146;
Best Local Similarity 67.5%; Pred. No. 8e-46;
Matches 108; Conservative 12; Mismatches 15; Indels 25; Gaps 3;

QY 1 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 6 MDWTWRLFLVAAATGAHSQVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWVGRINPNSGATDYAHKFQGRVTMSRDTISITAYMELSLRLTSDDT 120
Db 56 YDINWVRQATGQGLEWVGRINPNSANTGYAQKFGRTVTRNTSISTAYMELSLRLTSDDT 115
QY 121 AMYICARADNY-----FDIVTGYTSHYFDYWGRTLVTV 154
Db 116 AVYICARRRRWELLGWMWD-----FDYWGQGLIVTV 146
```

```
; Patent No. US20020122807A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-09-747-669-3

Query Match      64.5%; Score 540; DB 9; Length 476;
Best Local Similarity 88.8%; Pred. No. 3.5e-45;
Matches 109; Conservative 14; Mismatches 20; Indels 16; Gaps 4;

QY 1 MDWTRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
DB 1 MDWTRVLFVLAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSLRSDDT 120
DB 1 MDWTRVLFVLAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
QY 121 AMYICAR-ADNYFDIVGTSHYP--DYMGRTGLTVSS 156
DB 111 AVYFCARNADN---VEMAAIHYHYGMDVWGQGTITVSS 146

; RESULT 6
; US-10-290-703-3
; Sequence 3, Application US/10290703
; Publication No. US20030118593A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-10-290-703-3

Query Match      64.5%; Score 540; DB 14; Length 476;
Best Local Similarity 68.6%; Pred. No. 3.5e-45;
Matches 109; Conservative 14; Mismatches 20; Indels 16; Gaps 4;
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```
QY 1 MDWTRILFLVAAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
DB 1 MDWTRVLFVLAATGAHSQVLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSLRSDDT 120
DB 51 FDLNWRVQAPGQGLEWMGRINPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSLRSDDT 110
QY 121 AMYICAR-ADNYFDIVGTSHYP--DYMGRTGLTVSS 156
DB 111 AVYFCARNADN---VEMAAIHYHYGMDVWGQGTITVSS 146

; RESULT 7
; US-09-880-748-1722
; Sequence 1722, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1722
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1722

Query Match      64.4%; Score 539; DB 10; Length 250;
Best Local Similarity 75.9%; Pred. No. 2.1e-45;
Matches 104; Conservative 10; Mismatches 13; Indels 10; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 79
DB 1 QVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 50
QY 80 INPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSLRSDDTSTAYMELSLRSDDTSTAYMELSLRSDDT 139
DB 51 INPNSGATDYAHKFGQGVTVMSRDTSTSTAYMELSLRSDDTSTAYMELSLRSDDTSTAYMELSLRSDDT 110
QY 140 SHYFDYMGRTGLTVSS 156
DB 111 QNWFDPMGRGLTVSS 127

; RESULT 8
; US-10-390-986-8
; Sequence 8, Application US/10390986
; Publication No. US20030166011A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: JI-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
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; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-8

Query Match      63.6%; Score 532; DB 14; Length 149;
Best Local Similarity 68.6%; Pred. No. 5.7e-45;
Matches 107; Conservative 9; Mismatches 26; Indels 14; Gaps 2;

QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKPKGASVKVCKTSGYNFTGYSGASGHIFTA 60
   |||||
Db 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKPKGASVKVCKAFWL-----HLSPG 51
   |||||

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRSDDT 120
   |||||
Db 52 YMHVVRQAPGQGLEWMGRINPNSGTHYAQMFQGRVTVTRDTSTAYMELSLRSDDT 111
   |||||

QY 121 AMYYCARADNYFDIVTGYTSHYFDYKRGTLTVSS 156
   |||||
Db 112 AVYYCAR-----EGIAAAAIYGMVWGQGTITVSS 142
   |||||

RESULT 9
US-09-880-748-1723
; Sequence 1723, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1723
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1723

Query Match      63.0%; Score 527; DB 10; Length 250;
Best Local Similarity 73.0%; Pred. No. 3.3e-44;
Matches 100; Conservative 14; Mismatches 13; Indels 10; Gaps 1;

QY 20 QVQLVQSGAEVKPKGASVKVCKTSGYNFTGYSGASGHIFTAYSVHWVRQAPGQGLEWMGR 79
   |||||
Db 1 EVQLQSGAEVKPKGASVKVCKSGYTFGT-----YMHVVRQAPGQGLEWMGW 50
   |||||

QY 80 INPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRSDDTTAMYYCARADNYFDIVTGYT 139
   |||||
Db 51 INPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRSDDTTAVYYCARVPHYDILTQYS 110
   |||||

QY 140 SHYFDYKRGTLTVSS 156
   |||||
Db 111 QNWFDPWKGKGMVTVSS 127
   |||||
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RESULT 10
US-10-390-986-12
; Sequence 12, Application US/10390986
; Publication No. US2003018601A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-12

Query Match      62.8%; Score 525.5; DB 14; Length 146;
Best Local Similarity 67.3%; Pred. No. 2.5e-44;
Matches 105; Conservative 9; Mismatches 25; Indels 17; Gaps 2;

QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKPKGASVKVCKTSGYNFTGYSGASGHIFTA 60
   |||||
Db 1 MDCWTRIFLVAATGTHAQVQLVQSGAEVKPKGASVKVCKSGYV-----LIE 50
   |||||

QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTSTAYMELSLRSDDT 120
   |||||
Db 51 LSMHWVRQAPGKGLEWMSFDPEDGETIYAKFGQRTVMTEDTSTDTAYMELSLRSED 110
   |||||

QY 121 AMYYCARADNYFDIVTGYTSHYFDYKRGTLTVSS 156
   |||||
Db 111 AVYYCATS-----TVTPWYFDYWGQGLTVTVSS 139
   |||||

RESULT 11
US-09-880-748-1640
; Sequence 1640, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1640

Query Match      62.8%; Score 525.5; DB 10; Length 256;
Best Local Similarity 74.3%; Pred. No. 4.7e-44;
Matches 104; Conservative 8; Mismatches 15; Indels 13; Gaps 2;
```


QY 20 QVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQLEWNGR 79
Db 1 QVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTAYSVHWVRQAPGQLEWNGW 50
QY 80 INPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLTSDDTAMYYCARADNYFDIVTGY- 138
Db 51 INPNSGGTNYAQKFGQRTVMSRDTSTSTAYMELSLTSDDTAMYYCARADNYFDIVTGY 110
QY 139 --TSHVFDYWGRTGLTVTVSS 156
Db 111 RPEDGYFDYWGRTGLTVTVSS 130

RESULT 12
US-09-269-921-123
; Sequence 123, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; EARLIER FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 123
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region
; OTHER INFORMATION: version p
US-09-269-921-123

Query Match 62.5%; Score 523.5; DB 10; Length 139;
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels 17; Gaps 3;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTRVFFLLAVAPGAHSGVQLVQSGAEVKKPGASVKVCKASGYT-----FTP 50
QY 61 YSVHWVRQAPGQLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLTSDDT 120
Db 51 YMWQVVRQAPGQLEWNGSIFPGDGTTRYSQKFGKRVMTADTSTSTAYMELSLRSED 110
QY 121 AMYCARADNYFDIVTGYTSHYFDYWGRTGLTVTVSS 156
Db 111 AVYICARG-----LRRG--GYFDYWGQGTITTVTVSS 139

RESULT 13
US-09-509-098-46
; Sequence 46, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02

; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized H chain V
; OTHER INFORMATION: region (version p) of anti-HM 1.24 antibody
US-09-509-098-46

Query Match 62.5%; Score 523.5; DB 10; Length 139;
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels 17; Gaps 3;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTRVFFLLAVAPGAHSGVQLVQSGAEVKKPGASVKVCKASGYT-----FTP 50
QY 61 YSVHWVRQAPGQLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLTSDDT 120
Db 51 YMWQVVRQAPGQLEWNGSIFPGDGTTRYSQKFGKRVMTADTSTSTAYMELSLRSED 110
QY 121 AMYCARADNYFDIVTGYTSHYFDYWGRTGLTVTVSS 156
Db 111 AVYICARG-----LRRG--GYFDYWGQGTITTVTVSS 139

RESULT 14
US-10-218-253-123
; Sequence 123, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 123
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region
; OTHER INFORMATION: version p
US-10-218-253-123

Query Match 62.5%; Score 523.5; DB 14; Length 139;
Best Local Similarity 66.7%; Pred. No. 3.7e-44;
Matches 104; Conservative 11; Mismatches 24; Indels 17; Gaps 3;
QY 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVCKTSGYNFTGYSASGHIFTA 60
Db 1 MDWTRVFFLLAVAPGAHSGVQLVQSGAEVKKPGASVKVCKASGYT-----FTP 50
QY 61 YSVHWVRQAPGQLEWNGRINPNSGATDYAHKFGQRTVMSRDTSTSTAYMELSLTSDDT 120
Db 51 YMWQVVRQAPGQLEWNGSIFPGDGTTRYSQKFGKRVMTADTSTSTAYMELSLRSED 110

Qy 121 AMYYCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
|:|||||:|:|||||:|||||
Db 111 AVTYCARG-----LRRG--GYFDYWGQGTIVTVSS 139

RESULT 15

US-10-390-986-10
; Sequence 10, Application US/10390986
; Publication No. US2003016601A1
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/10/390,986
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/582,337
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-986-10

Query Match 62.5%; Score 523.5; DB 14; Length 146;
Best Local Similarity 67.3%; Pred. No. 3.9e-44;
Matches 105; Conservative 9; Mismatches 25; Indels 17; Gaps 2;

Qy 1 MDWTWRIFLVAATGAHSQVLVQSGAEVKKPGASVKVCKTSQGYNFTGYSASGHIFTA 60
|:|||||:|:|||||:|||||:|||||
Db 1 MDCTWRIFLVAATGTHAQVLVQFGAEVKKPGASVKVCKVSGYT-----LFE 50
Qy 61 YSVHWVRQAPCGQGLEWNGRINPNSGATDYAHKFGQGRVTMSRDTISITAYNELSLTSDDT 120
|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 51 LSMHWVRQAPCGKGLEWNGSFDPEDGETIYAQKFGQGRVTMTDTSTAYNELSLRSEDT 110
Qy 121 AMYYCARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
|:|||||:|:|||||:|||||:|||||
Db 111 AVTYCATS-----TVTPWYFDYWGQGTIVTVSS 139

Search completed: April 5, 2004, 13:59:14
Job time : 37.6904 secs


```

; CLONE: 3551457
US-09-049-672A-13

Query Match      65.8%; Score 550.5; DB 3; Length 236;
Best Local Similarity 70.7%; Pred. No. 1.3e-48;
Matches 111; Conservative 13; Mismatches 14; Indels 19; Gaps 4;

QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
   |||
Db 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
   |||
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRSDDT 120
   |||
Db 51 YAMHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRSDDT 110
   |||
QY 121 AMYTCARADNYFDIVTG-VTSHYFDYWGRTLVTVSS 156
   |||
Db 111 AVTYCAR-----VWAGEFTS--FDWQQGTLTVTVSS 139
   |||

RESULT 2
US-08-545-809A-90
; Sequence 90, Application US/08545809A
; Patent No. 6098878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA: PCT/JP93/00603
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-90

Query Match      65.7%; Score 550; DB 3; Length 117;
Best Local Similarity 83.5%; Pred. No. 6.1e-49;
Matches 106; Conservative 4; Mismatches 7; Indels 10; Gaps 1;

QY 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
   |||
Db 1 MDWTWRIFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
   |||
QY 61 YSVHWVRQAPGQGLEWMGRINPNSGATDYAHKFGQRTVMSRDTISITAYMELSLRSDDT 120
   |||

Query Match      62.8%; Score 525.5; DB 4; Length 146;
Best Local Similarity 67.3%; Pred. No. 2.6e-46;

```


APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: EDA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-968-38

Query Match 61.8%; Score 517.5; DB 3; Length 137;
Best Local Similarity 64.1%; Pred. No. 1.6e-45;
Matches 100; Conservative 15; Mismatches 22; Indels 19; Gaps 2;

QY 1 MDWTRILFLVAATGASHQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
DB 1 MDWTRVFCLLAVAPGASHQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTE 50
QY 61 YSVHWVROAPGQGLEWNGRINPNSGATDYAHKFGQGRVTMSRDTSTAYMELSLRSTDDT 120
DB 51 YTHHWVRQAPGQGLEWNGRINPNSGATDYAHKFGQGRVTMSRDTSTAYMELSLRSTDDT 110
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
DB 111 AVYICA-----TPYVAIDSMGQGLTVTVSS 137

RESULT 10
US-09-355-925-7
Sequence 7, Application US/09355925
Patent No. 6503510

GENERAL INFORMATION:
APPLICANT: KOISHIHARA, YASUO
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 139
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of H chain V region version r of
OTHER INFORMATION: humanized anti-HM1.24 antibody

US-09-355-925-7
Query Match 61.8%; Score 517.5; DB 4; Length 139;
Best Local Similarity 66.0%; Pred. No. 1.6e-45;
Matches 103; Conservative 11; Mismatches 25; Indels 17; Gaps 3;

QY 1 MDWTRILFLVAATGASHQVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTA 60
DB 1 MDWTRVFCLLAVAPGASHQVQLVQSGAEVKKPGASVKVSCKASGYT-----FTP 50

QY 61 YSVHWVROAPGQGLEWNGRINPNSGATDYAHKFGQGRVTMSRDTSTAYMELSLRSTDDT 120
DB 51 YHWVROAPGQGLEWNGSIFPGDTRYSQKFGRTVMTADKSTSTAYMELSLRSEDT 110
QY 121 AMYICARADNYFDIVTGYTSHYFDYWGRTLVTVSS 156
DB 111 AVYICARG-----LRRG--GYFDYWGQGLTVTVSS 139

RESULT 11

US-08-477-877B-94
Sequence 94, Application US/08477877B
Patent No. 5730979

GENERAL INFORMATION:
APPLICANT: Bazin, Herv
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cecelia, Byrne, Bain, Gilfillan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,877B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.

US-08-477-877B-94

Query Match 61.6%; Score 516; DB 1; Length 123;
Best Local Similarity 74.5%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 13; Indels 14; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKTSQYNFTGYSASGHIFTAYSVHWVROAPGQGLEWNGR 79
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTG-----YHWHVROAPGQGLEWNGR 50
QY 80 INPNSGATDYAHKFGQGRVTMSRDTSTAYMELSLRSTDDTAMYYICARADNYFDIVTGYT 139
DB 51 INPNSGGINYYAKQKFGQGRVTMTSDTSTAYMELSLRSDDTAVYICARGTEYIVV---- 106

QY 140 SHYFDYWGRTLVTVSS 156
Db 107 AEGFDYWGQGLTVTVSS 123

RESULT 12

US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latime, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-472-281A-94

Query Match 61.6%; Score 516; DB 2; Length 123;
Best Local Similarity 74.5%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 13; Indels 14; Gaps 2;
QY 20 QVQLVQSGAEVKPGASVKVSCKTSYINFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 79
Db 1 QVQLVQSGAEVKPGASVKVSCKASGYTFG-----YYMHVVRQAPGQGLEWMGR 50
QY 80 INPNSGATDYAHKFGQGVMTSRDTSISTAYMELSLTSDDTAMYCARADNYFDIVTGYT 139
Db 51 INPNSGNTYAQKFGQGVMTSRDTSISTAYMELSLRSLSDDTAVYICARGTEYIVV---- 106
QY 140 SHYFDYWGRTLVTVSS 156
Db 107 AEGFDYWGQGLTVTVSS 123

RESULT 13

US-08-477-989B-94
; Sequence 94, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latime, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable
; NAME/KEY: region.
; US-08-477-989B-94

Query Match 61.6%; Score 516; DB 2; Length 123;
Best Local Similarity 74.5%; Pred. No. 2e-45;
Matches 102; Conservative 8; Mismatches 13; Indels 14; Gaps 2;
QY 20 QVQLVQSGAEVKPGASVKVSCKTSYINFTGYSASGHIFTAYSVHWVRQAPGQGLEWMGR 79
Db 1 QVQLVQSGAEVKPGASVKVSCKASGYTFG-----YYMHVVRQAPGQGLEWMGR 50
QY 80 INPNSGATDYAHKFGQGVMTSRDTSISTAYMELSLTSDDTAMYCARADNYFDIVTGYT 139
Db 51 INPNSGNTYAQKFGQGVMTSRDTSISTAYMELSLRSLSDDTAVYICARGTEYIVV---- 106
QY 140 SHYFDYWGRTLVTVSS 156

Mon Apr 5 14:16:20 2004

us-10-044-569b-6.rai

Page 8

Search completed: April 5, 2004, 13:44:09
Job time : 14.9898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:25:01 ; Search time 11.6142 Seconds
(without alignments)
1184.358 Million cell updates/sec

Title: US-10-044-569B-8
Perfect score: 738
Sequence: 1 METPAQLLFLLLWLPLEDTTG.....TKVEIKRTVAAPSVFIFFPS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625.5	84.8	145	2 S20631	IG kappa chain - h
2	619	83.9	144	2 PL0106	IG kappa chain pre
3	608.5	82.5	129	1 K3HUHA	IG kappa chain pre
4	598.5	81.1	129	1 K3HUHI	IG kappa chain pre
5	596.5	80.8	129	2 S49532	anti-Sm antibody V
6	590.5	80.0	128	2 S20636	IG kappa chain V r
7	585.5	79.3	129	2 S46369	IG light chain var
8	585.5	79.3	134	2 S38643	IG kappa chain V r
9	576	78.0	129	2 S40325	IG kappa chain - h
10	572.5	77.6	129	2 A32274	IG kappa chain pre
11	570.5	77.3	130	2 S20637	IG kappa chain V r
12	569	77.1	131	2 S40346	IG kappa chain V-J
13	566.5	76.8	130	2 S40360	IG kappa chain - h
14	564	76.4	116	2 B27594	IG kappa chain pre
15	563.5	76.4	121	2 S40327	IG kappa chain - h
16	552.5	74.9	116	2 C27594	IG kappa chain pre
17	548.5	74.3	124	2 S20633	IG kappa chain - h
18	537	72.8	116	2 B25521	IG kappa chain pre
19	535	72.5	128	1 K3HU41	IG kappa chain pre
20	533.5	72.3	127	2 S40380	IG kappa chain pre
21	533.5	72.3	129	2 S40363	IG kappa chain V-J
22	532.5	72.2	215	2 A23746	IG kappa chain - h
23	531	72.0	129	2 S29627	IG kappa chain V r
24	527	71.4	128	2 S40379	IG kappa chain V-J
25	526	71.3	114	2 S46375	IG kappa chain V-J
26	525	71.1	125	2 S40344	IG kappa chain V-J
27	525	71.1	128	2 S40345	IG kappa chain V-J
28	524	71.0	128	2 A56701	IG kappa chain V r
29	519.5	70.4	215	2 JE0242	IG kappa chain NIG

30 518 70.2 128 2 S40343 IG kappa chain V-J
31 510.5 69.2 109 2 A30608 IG kappa chain V-I
32 510.5 69.2 131 2 S40328 IG kappa chain - h
33 506.5 68.6 115 1 K3HUVG IG kappa chain pre
34 506.5 68.6 215 2 JE0244 IG kappa chain NIG
35 505.5 68.5 109 2 B30601 IG kappa chain V-I
36 503 68.2 116 1 K3HUVH IG kappa chain pre
37 503 68.2 116 2 S41817 IG kappa chain V r
38 502.5 68.1 109 2 C30601 IG kappa chain V-I
39 501.5 68.0 109 2 G30607 IG kappa chain V-I
40 501 67.9 110 2 E30607 IG kappa chain V-I
41 501 67.9 111 2 S40359 IG kappa chain V-J
42 499.5 67.7 109 2 D30601 IG kappa chain V-I
43 499 67.6 108 2 H44151 IG kappa chain V r
44 497.5 67.4 109 2 H30601 IG kappa chain V-I
45 494.5 67.0 109 2 G30601 IG kappa chain V-I

ALIGNMENTS

RESULT 1

S20631
IG kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20631
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20631
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <LEE>
A:Cross-references: EMBL:Z11903; NID:G33156; PIDN:CAA77955.1; PID:G33157
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMW>

Query Match 84.8%; Score 625.5; DB 2; Length 145;
Best Local Similarity 86.0%; Pred. No. 1.3e-44;
Matches 123; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

Qy 1 METPAQLLFLLLWLPLEDTTG...TKVEIKRTVAAPSVFIFFPS 143
Db 1 METPAQLLFLLLWLPLEDTTG...TKVEIKRTVAAPSVFIFFPS 142

Qy 61 PGQAPRLIIYGASRATDIPHRFGSGSGTDFLTISRLEPEDFAVYVCOQYGTSLTF 120
Db 61 PGQAPSLVIYGVIRATGIDRFSGSGSETDFTLTISRLEPEDFAVYVCHQGYTP-LTF 119

Qy 121 GGGTKVEIKRTVAAPSVFIFFPS 143
Db 120 GGGTKVEIKRTVAAPSVFIFFPS 142

RESULT 2

PL0106
IG kappa chain precursor V-J-C region (LS1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: PL0106; MUID:89235583; PMID:2341221
A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SLT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>

```
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match      83.9%; Score 619; DB 2; Length 144;
Best Local Similarity 88.1%; Pred. No. 4.4e-44;
Matches 126; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
Db 1 MEAPQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQOR 59
   |||||

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITLF 120
   |||||
Db 60 PGQAPRLIIYDASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYCCQ-RSNWPLTF 118
   |||||

QY 121 GGQTKVEIKRTVAAPSVFIFPPS 143
   |||||
Db 119 GGQTKVEIKRTVAAPSVFIFPPS 141
   |||||

RESULT 3
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0022
R:Kippes, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JKL)
F:43-109/Disulfide bonds: #status predicted

Query Match      82.5%; Score 608.5; DB 1; Length 129;
Best Local Similarity 93.1%; Pred. No. 2.9e-43;
Matches 121; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
   |||||

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITLF 120
   |||||
Db 61 PGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSP-RTF 119
   |||||

Query Match      80.8%; Score 596.5; DB 2; Length 129;
Best Local Similarity 90.8%; Pred. No. 2.8e-42;
Matches 118; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
```

```
RESULT 4
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0021
R:Kippes, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0021
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JKL)
F:43-109/Disulfide bonds: #status predicted

Query Match      81.1%; Score 598.5; DB 1; Length 129;
Best Local Similarity 91.3%; Pred. No. 1.9e-42;
Matches 119; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOK 60
   |||||

QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITLF 120
   |||||
Db 61 PGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119
   |||||

QY 121 GGQTKVEIKR 130
   |||||
Db 120 GGQTKVEIKR 129
   |||||

RESULT 5
S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C:Accession: S49532
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49532
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <MAH>
A:Cross-references: EMBL:Z46345; NID:G560843; PID:CAA86464.1; PID:G560844
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 596.5; DB 2; Length 129;
Best Local Similarity 90.8%; Pred. No. 2.8e-42;
Matches 118; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPATLSLSPGERATLSCRASQSVASAYLAWYQOK 60
   |||||
```

Db 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
QY 61 PQGAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQGAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 119
QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 6

S20636
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20636
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Reference number: S20631
A;Accession: S20636
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <BEN>
A;Cross-references: EMBL:Z11894; NID:G33200; PIDN:CAA77948.1; PID:G33201
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 590.5; DB 2; Length 128;
Best Local Similarity 91.5%; Pred. No. 8.7e-42;
Matches 118; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
Db 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
QY 61 PQGAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQGAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 119

QY 121 GGGTKVEIKR 129
Db 120 GGGTKVEIKR 128

RESULT 7

S46369
IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S46369
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
A;Reference number: S46369; MUID:94313975; PMID:8039491

A;Accession: S46369
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <BEN>
A;Cross-references: EMBL:Z27170
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 585.5; DB 2; Length 129;
Best Local Similarity 88.5%; Pred. No. 2.3e-41;
Matches 115; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
Db 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60

QY 61 PQGAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 61 PQGAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 119
QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 8

S38643
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38643
R;Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <BEN>
A;Cross-references: EMBL:Z27170; NID:G415955; PIDN:CAA81694.1; PID:G415956
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;41-116/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 585.5; DB 2; Length 134;
Best Local Similarity 88.5%; Pred. No. 2.3e-41;
Matches 115; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 60
Db 6 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOK 65
QY 61 PQGAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
Db 66 PQGAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 124
QY 121 GGGTKVEIKR 130
Db 125 GGGTKVEIKR 134

RESULT 9

S40325
IG kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40325
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40325
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72435; NID:G441338; PIDN:CAA51103.1; PID:G441339
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;35-110/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 576; DB 2; Length 129;
Best Local Similarity 84.5%; Pred. No. 1.4e-40;
Matches 109; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 2 ETPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRASQSSSYLAAYQOKP 61
Db 1 ETPAQLLFLLMLPDPSPGQVLTQSPVLTSLSPGERATLSCRASQSSSYLAAYQORP 60
QY 62 GQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 121

Db 61 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSLTFG 120
QY 122 GGTKEIKR 130
Db 121 PGTKVDIR 129

RESULT 10

A32274
Ig kappa chain precursor V-III region (EVI-15) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C:Accession: A32274
R:Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1516, 1988
A:Title: Complete protein sequences of the variable regions of the cloned heavy and light
actors of the wa idiotype family.
A:Reference number: A92767; MUID:88213701; PMID:2452836
A:Accession: A32274
A:Molecule type: DNA
A:Residues: 1-129 <NEW>
A:Cross-references: GB:W20031
A:Note: this sequence was determined from the codon GAT for residue 17 as Ala
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region EVI-15 #status predicted <KV3>
F:36-111/Domain: immunoglobulin homology <IMW>

Query Match 77.6%; Score 572.5; DB 2; Length 129;
Best Local Similarity 89.2%; Pred. No. 2.6e-40;
Matches 116; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 METPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVSSNELAWYQOK 60
QY 61 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSLTFG 120
Db 61 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSLTFG 119

QY 121 GGTKEIKR 130
Db 120 GGTKEIKR 129

RESULT 11

S20637
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20637; S20632
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20637
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <LEE>
A:Cross-references: EMBL:Z11890; NID:G33202; PIDN:CAA77944.1; PID:G33203; EMBL:Z11895; N
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMW>

Query Match 77.3%; Score 570.5; DB 2; Length 130;
Best Local Similarity 87.7%; Pred. No. 3.9e-40;
Matches 114; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 1 METPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSLTSNYLAWYQOK 60

QY 61 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSL-LT 119
Db 61 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSL-LT 120
QY 120 GGTKEIKR 129
Db 121 GGTKEIKR 130

RESULT 12

S40346
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40346
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40346
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72456; NID:9441380; PIDN:CAA51124.1; PID:9441381
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-110/Domain: immunoglobulin homology <IMW>

Query Match 77.1%; Score 569; DB 2; Length 131;
Best Local Similarity 84.0%; Pred. No. 5.2e-40;
Matches 110; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 ETPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 61
Db 1 ETPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVSSSELAWYQOK 60

QY 62 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSLTFG 121
Db 61 GQAPRLIIYGASRRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSLTFG 120

QY 122 GGTKEIKR 132
Db 121 GGTKEIKR 131

RESULT 13

S40360
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40360
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40360
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-130 <KLE>
A:Cross-references: EMBL:X72470; NID:9441408; PIDN:CAA51138.1; PID:9441409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-111/Domain: immunoglobulin homology <IMW>

Query Match 76.8%; Score 566.5; DB 2; Length 130;
Best Local Similarity 86.9%; Pred. No. 8.3e-40;
Matches 113; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 2 ETPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 ETPAQLFLLLLWLPDPTTGTEIVLTQPGTSLSPGERATLSCRASQSVYNNNLGWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGT 120
DB 61 PGQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGT 120
QY 121 GGGTKVEIKR 130
DB 121 GGGTKVEIKR 130

RESULT 14

B27594
IG kappa chain precursor V-III (Nalm-6) - human
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: B27594
R:Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J.
J. Exp. Med. 167, 488-501, 1988
A>Title: The kappa-deleting element. Germline and rearranged, duplicated and dispersed
A:Reference number: A92779; MUID:88154739; PMID:3126251
A:Accession: B27594
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-116 <GRA>
A>Note: this sequence was translated from an aberrantly rearranged kappa gene from lambda
C:Genetics:
A:Map position: 2
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 564; DB 2; Length 116;
Best Local Similarity 94.8%; Pred. No. 1.2e-39;
Matches 109; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 METPAQLLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTS 115
DB 61 PGQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSS 115

RESULT 15

S40327
IG kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40327
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40327
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72437; NID:G441342; PIDN:CAAS1105.1; PID:G441343
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-108/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 563.5; DB 2; Length 121;
Best Local Similarity 90.2%; Pred. No. 1.4e-39;
Matches 110; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 4 PAQLFLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOKPQ 63
DB 1 PAQLFLLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVSSYLAWYQOKPQ 60

QY 64 APRLLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTALLTFGGG 123

DB 61 APRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSP-ITFGQG 119
QY 124 TK 125
DB 120 TR 121

Search completed: April 5, 2004, 13:43:03
Job time : 12.6142 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:10:21 ; Search time 6.533 Seconds
(without alignments)
1139.758 Million cell updates/sec

Title: US-10-044-569B-8

Perfect score: 738

Sequence: 1 METPAQLFLLLMLPDTTG.....TKVEIKRTVAAPSVFIFFPS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608.5	82.5	129	1	KV3L_HUMAN
2	598.5	81.1	129	1	KV3M_HUMAN
3	535	72.5	128	1	KV3K_HUMAN
4	531.5	72.0	129	1	KV3H_HUMAN
5	506.5	68.6	115	1	KV3I_HUMAN
6	503	68.2	116	1	KV3J_HUMAN
7	489.5	66.3	109	1	KV3E_HUMAN
8	489.5	66.3	109	1	KV3E_HUMAN
9	481.5	65.2	109	1	KV3D_HUMAN
10	464.5	62.9	109	1	KV3G_HUMAN
11	457.5	62.0	108	1	KV3A_HUMAN
12	456	61.8	100	1	KV3C_HUMAN
13	422.5	57.2	109	1	KV3F_HUMAN
14	417.5	56.6	123	1	KV4E_HUMAN
15	404	54.7	129	1	KV1W_HUMAN
16	399	54.1	134	1	KV4C_HUMAN
17	396.5	53.7	117	1	KV1J_HUMAN
18	393	53.3	131	1	KV2I_MOUSE
19	391.5	53.0	133	1	KV2F_MOUSE
20	379	51.4	129	1	KV1X_HUMAN
21	378	51.2	122	1	KV3F_MOUSE
22	378	51.2	149	1	KV5A_MOUSE
23	370	50.1	107	1	KV1Y_HUMAN
24	369.5	50.1	108	1	KV1D_HUMAN
25	367	49.7	108	1	KV1M_HUMAN
26	367	49.7	114	1	KV4A_HUMAN
27	365	49.5	128	1	KV5E_MOUSE
28	364	49.3	108	1	KV1H_HUMAN
29	363.5	49.3	121	1	KV40_HUMAN
30	358	48.5	136	1	KV5B_MOUSE
31	357	48.4	108	1	KV1F_HUMAN
32	356	48.2	108	1	KV1K_HUMAN
33	352	47.7	108	1	KV1S_HUMAN

P01601 homo sapien
P04430 homo sapien
P01608 homo sapien
P01610 homo sapien
P01597 homo sapien
P01604 homo sapien
P06309 homo sapien
P01664 mus musculus
P01666 mus musculus
P01609 homo sapien
P01673 mus musculus
P01612 homo sapien

ALIGNMENTS

RESULT 1

KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.

AC P18135;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region HAH precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=88171307; PubMed=3127527;

RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;

RT "Autoantibody-associated kappa light chain variable region gene

expressed in chronic lymphocytic leukemia with little or no somatic

mutation. Implications for etiology and immunotherapy.";

RL J. Exp. Med. 167:840-852(1988).

CC -I- DISEASE: The protein is one of the surface immunoglobulin M

autoantibodies expressed in patients with chronic lymphocytic

leukemia.

CC PIR; P00022; K3HUHA.

DR HSSP; P80362; 1WTL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS00835; IG LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 56 70 FRAMEWORK-2.

FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 78 109 FRAMEWORK-3.

FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 119 129 JK1 SEGMENT.

FT DISULFID 43 109 BY SIMILARITY.

FT NON_TER 129

SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 82.5%; Score 608.5; DB 1; Length 129;

Best Local Similarity 93.1%; Pred. No. 7.5e-52;

Matches 121; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 1 METPAQLFLLLMLPDTTGIVLTQPGTSLSPGERATLSCRASQSVASVLAAYQOK 60

Db 1 METPAQLFLLLMLPDTTGIVLTQPGTSLSPGERATLSCRASQSVASVLAAYQOK 60

Qy 61 PGQAPRLIYGAASSRATDIPHRFSGSGSGTDFLTITSLRLEPEDFAVYCCQYGTGTSALLTF 120

Db 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDPAVYVCOQYGTSP-RTF 119

QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 2

KV3M HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HIC precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tonhave E., Chen P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.

DR PIR: P18021; K3HUH1.
DR HSSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 129 129
SQ SEQUENCE 129 AA; 7395528EA2BB74D6 CRC64;

Query Match 81.1%; Score 598.5; DB 1; Length 129;
Best Local Similarity 91.5%; Pred. No. 6.9e-51;
Matches 119; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
QY 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPIHRFSGSGGTDFLTISRLEPEDPAVYVCOQYGTSP-RTF 120

Db 61 PGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDPAVYVCOQYGTSP-WTF 119

QY 121 GGGTKVEIKR 130
Db 120 GGGTKVEIKR 129

RESULT 3

KV3H HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;

KV3K HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).

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DR EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.5%; Score 535; DB 1; Length 128;
Best Local Similarity 85.4%; Pred. No. 9e-45;
Matches 111; Conservative 3; Mismatches 14; Indels 2; Gaps 2;
QY 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQOK 59

QY 61 PGQAPRLIYGASSRATDIPIHRFSGSGGTDFLTISRLEPEDPAVYVCOQYGTSP-RTF 120

Db 60 RGQAPRLIIRPSSRANGIPDRFSGSGGTDFLTISRLEPEDPAVYVCOQYGTSP-YTF 118

QY 121 GGGTKVEIKR 130
Db 119 GGGTKLEIKR 128

RESULT 4

KV3H HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;

DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177570; PubMed=3083417;
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199 (1986).
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 CC -----
 DE EMBL; M12740; AA858992.1; -;
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IG; 1.
 DR Pfam; PF00047; Ig; 1.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
 Query Match 72.0%; Score 531.5; DB 1; Length 129;
 Best Local Similarity 82.3%; Pred. No. 2e-44;
 Matches 107; Conservative 6; Mismatches 16; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLWLPDPTTGTGEIVLTQPGTSLSPGERATLSRASCQSVASAYLAWYQOK 60
 DB 1 MEAPAQLLFLLLLWLPDPTTGTGEIVLTQSPATLSLSPGERATLSRASCQSV-SNNLAWYQOK 59
 QY 61 PGQAPRLIYGASSRATDIPHRFGSGSGTDFLTISRLPEPFAVYCCQYQYQYQYQYQY 120
 DB 60 PGQAPRLIYGASTRATGIPARFGSGSGTDFLTISRLQSEDFAVYCCQYQYQYQYQYQY 119
 QY 121 GGGTKVEIKR 130
 DB 120 GGGTRVEIKR 129
 RESULT 5
 KV31_HUMAN STANDARD; PRT; 115 AA.
 ID KV31_HUMAN
 AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus.";
 RL Nucleic Acids Res. 12:9229-9236 (1984).
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 CC -----
 DE EMBL; X01668; -; NOT_ANNOTATED_CDS.
 DR PIR; A01900; K3HUVG.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IG; 1.
 DR Pfam; PF00047; Ig; 1.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
 Query Match 68.6%; Score 506.5; DB 1; Length 115;
 Best Local Similarity 91.0%; Pred. No. 4.4e-42;
 Matches 101; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLWLPDPTTGTGEIVLTQPGTSLSPGERATLSRASCQSVASAYLAWYQOK 60
 DB 1 MEAPAQLLFLLLLWLPDPTTGTGEIVLTQSPATLSLSPGERATLSRASCQSV-SSYLAWYQOK 59
 QY 61 PGQAPRLIYGASSRATDIPHRFGSGSGTDFLTISRLPEPFAVYCCQ 111
 DB 60 PGQAPRLIYGASTRATGIPARFGSGSGTDFLTISRLPEPFAVYCCQ 110
 RESULT 6
 KV31_HUMAN STANDARD; PRT; 116 AA.
 ID KV31_HUMAN
 AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VH precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;

RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RL within the VK locus."
RL Nucleic Acids Res. 12:9229-9236 (1984).
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DR EMBL: X02725; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSP: P80362; IWTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 68.2%; Score 503; DB 1; Length 116;
Best Local Similarity 87.4%; Pred. No. 9.7e-42;
Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 METAQALLLLMLPDTTQIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQQK 60
DB 1 METAQALLLLMLPDTTQIVLTQPGTILSPGERATLSCRASQSVSSYLTWYQQK 60
QY 61 PQQAPRLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQ 111
DB 61 PQQAPRLIYGASTRATSPARFSGSGSGTDFLTISRLEPEDFAVYCCQ 111

RESULT 7
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SI.E.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
PIR: A01892; K3HUSI.

DR HSP: P80362; IWTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
DR Immunoglobulin V region.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 66.3%; Score 489.5; DB 1; Length 109;
Best Local Similarity 88.2%; Pred. No. 1.8e-40;
Matches 97; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
QY 21 EIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLIYGASSRATDIP 80
DB 1 EIVLTQPGTILSPGERATLSCRASQSVNSYLAQYQQKPGQAPRLIYGASSRATGIP 60
QY 81 HRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKR 130
DB 61 DRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKR 109

RESULT 8
KV3E_HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
PIR: A01896; K3HUL.
DR HSP: P80362; IWTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
DR Immunoglobulin V region.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CEEE CRC64;

Query Match 66.3%; Score 489.5; DB 1; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.8e-40;
Matches 99; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 21 EIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQQKPGQAPRLIYGASSRATDIP 80
DB 1 EIVLTQPGTILSPGERATLSCRASQSVSSYLTWYQQKPGQAPRLIYGASSRATGIP 60
QY 81 HRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSAALLTFGGTKVEIKR 130

```
Db 61 DRFGSGSGDTFTLTISRLEPEDFAVYCOQYG-SLGRFTGGTKVEIKR 109
|||||
RESULT 9
KV3D_HUMAN STANDARD; PRT; 109 AA.
ID KV3D_HUMAN
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUG1.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058DCD7749BC CRC64;

Query Match 65.2%; Score 481.5; DB 1; Length 109;
Best Local Similarity 87.3%; Pred. No. 1.1e-39;
Matches 96; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQQKPGAPRLIYVASSRATDIP 80
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVNSFLAWYQQKPGAPRLIYVASSRATGIP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 81 HRFSGSGGTFTLTISRLEPEDFAVYCOQYGTSAITFGGKVEIKR 130
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 DRFGSGSGDTFTLTISRLEPEDFAVYCOQYGGSP-STFGGKVEIKR 109
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
KV3G_HUMAN STANDARD; PRT; 109 AA.
ID KV3G_HUMAN
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
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RT reactivity with antipeptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR; A01893; K3HUGO.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 62.9%; Score 464.5; DB 1; Length 109;
Best Local Similarity 84.5%; Pred. No. 4.7e-38;
Matches 93; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQQKPGAPRLIYVASSRATDIP 80
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 EIVLTQPGTSLSPGERATLSCRAALLSSRGYLAWYQQKPGAPRLIYVASSRATGIP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 81 HRFSGSGGTFTLTISRLEPEDFAVYCOQYGTSAITFGGKVEIKR 130
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 DRFGSGSGGTFTLTISRLEPEDFAVYCOQYGGSP-RSFGGKVEIKR 109
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
KV3A_HUMAN STANDARD; PRT; 108 AA.
ID KV3A_HUMAN
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Igv_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 62.0%; Score 457.5; DB 1; Length 108;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 87; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQQKPGAPRLIYVASSRATDIP 80
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 ZIVLTZSPGTSLSPGERATLSCRAALSSRGYLAWYQQKPGAPRLIYVASSRATGIP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 81 HRFSGSGGTFTLTISRLEPEDFAVYCOQYGTSAITFGGKVEIKR 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 DRFGSGSGADTTLTISRLEPEDFAVYCOQYGGSP-FTFGGSKLEIK 108
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
```

```
RESULT 12
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
KW Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
KW Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FT DISULFID 23 89
FT NON_TER 109 109
SQ NCBI_TaxID=9606;
SEQUENCE 109 AA; 11922 MW; 62821DDC6A8AB86 CRC64;
Query Match 57.2%; Score 422.5; DB 1; Length 109;
Best Local Similarity 76.4%; Pred. No. 5.2e-34;
Matches 84; Conservative 11; Mismatches 14; Indels 1; Gaps 1;
RT 21 EIVTQFPGLTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSTRATDIP 80
DB 1 EIVMTQSPVTLTVSGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSTRATGIP 60
QY 81 HRFSGSGGTDTLTISRLPEDPFVYCCQYQVTSALLTFGGGKVKIKR 130
DB 61 ARFSGSGGTDTLTISRLPEDPFVYCCQYQVTSALLTFGGGKVKIKR 109
QY 81 HRFSGSGGTDTLTISRLPEDPFVYCCQYQVTSALLTFGGGKVKIKR 130
DB 61 ARFSGSGGTDTLTISRLPEDPFVYCCQYQVTSALLTFGGGKVKIKR 109
RESULT 14
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G.; Bornkamm G.W.; Combriato G.; Mocikat R.; Pohlenz H.D.;
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC -----
CC EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJ1.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133
FT DOMAIN 21 43
FT DOMAIN 44 60
QY 19 TGEIVLTQFRTLSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSTRATD 78
DB 3 SGEIVLTQFRTLSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIIYGASSTRATG 62
QY 79 IPRFSGSGGTDTLTISRLPEDPFVYCCQYQVTS 115
DB 63 IPRFSGSGGTDTLTISRLPEDPFVYCCQYQVTS 99
RESULT 13
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G.; Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
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FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match
Best Local Similarity 56.68; Score 417.5; DB 1; Length 133;
Matches 84; Conservative 18; Mismatches 26; Indels 7; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPPGTLSPGERATLSCRASQSVASA-----YLA 55
Db 1 MWLQTVFISLLWISGAYGDIWVTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA 60
QY 56 WYQKPGQAPRLIYGNSSRATDIPHRFSGSGGTDFTLTISLREDFAVYCCQYGT 115
Db 61 WYQKPGQAPRLIYGNSSRATDIPHRFSGSGGTDFTLTISLREDFAVYCCQYGT- 119
QY 116 ALLTFGGGKVEIKR 130
Db 120 -IPTFGGKVEIKR 133

RESULT 15
KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klocbeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006 (1984).
CC
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC PIR; A01883; KJHWK.
CC HSP; P01607; IREI.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR07110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IGLIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
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FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match
Best Local Similarity 54.78; Score 404; DB 1; Length 129;
Matches 83; Conservative 15; Mismatches 29; Indels 2; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPPGTLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 3 MRVPAQLGLLLWLARGARCDIQTSFSSLSASVGRVTITCRASQSI-SNYLWYQOK 61
QY 61 PQQAPRLIYGCASRATDIPHRFSGSGGTDFTLTISLREDFAVYCCQYGTSAITTF 120
Db 62 PKAPKLLIYAASSLSQSGVTSRFSGSGGTDFTLTISLQPEDSATYCCQ-SYSTLTTF 120
QY 121 GGGTKVEIK 129
Db 121 QGGTRLEIK 129
```

Search completed: April 5, 2004, 13:24:56
Job time : 7.533 secs

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OM protein - protein search, using sw model

Run on: April 5, 2004, 13:24:21 ; Search time 30.4873 Seconds
(without alignments)
1479.931 Million cell updates/sec

Title: US-10-044-569B-8
Perfect score: 738
Sequence: 1 METPAQLFLFLLLWLPDTTG.....TKVBIKRTVAAPSVFIIPPS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	505.5	68.5	109	Q9UL78	Q9UL78 homo sapien
2	483.5	65.5	109	Q9UL86	Q9UL86 homo sapien
3	479	64.9	234	Q7Z473	Q7Z473 homo sapien
4	460.5	62.4	239	Q8NEK0	Q8NEK0 homo sapien
5	455	61.7	236	Q7Z3V4	Q7Z3V4 homo sapien
6	443.5	60.1	229	Q8TCD0	Q8TCD0 homo sapien
7	436.5	59.1	109	Q9UL85	Q9UL85 homo sapien
8	418	56.6	237	Q7SZ36	Q7SZ36 xenopus lae
9	415	56.2	238	Q9NM37	Q9NM37 mus musculus
10	413	56.0	238	Q8VCI6	Q8VCI6 mus musculus
11	411	55.7	108	Q9UL83	Q9UL83 homo sapien
12	407	55.1	236	Q7TS98	Q7TS98 mus musculus
13	404	54.7	236	Q7TMK3	Q7TMK3 mus musculus
14	390.5	52.9	239	Q8K0F8	Q8K0F8 mus musculus
15	389	52.7	234	Q8VCP0	Q8VCP0 mus musculus
16	388.5	52.6	107	Q96SA9	Q96SA9 homo sapien

17	387.5	52.5	239	11	Q8VC55	Q8VC55 mus musculus
18	381	51.6	234	11	Q8R062	Q8R062 mus musculus
19	377	51.1	108	4	Q9UL77	Q9UL77 homo sapien
20	374	50.7	131	11	Q8LIC3	Q8LIC3 mus musculus
21	374	50.7	234	11	Q9IWF8	Q9IWF8 mus musculus
22	367	49.7	108	4	Q9UL79	Q9UL79 homo sapien
23	367	49.7	233	11	Q9IWS9	Q9IWS9 mus musculus
24	365.5	49.5	114	11	Q8K1F1	Q8K1F1 mus musculus
25	362.5	49.1	235	11	Q7TMK0	Q7TMK0 mus musculus
26	358.5	48.6	107	4	Q9UL81	Q9UL81 homo sapien
27	358	48.5	108	4	Q9UL70	Q9UL70 homo sapien
28	357	48.4	116	4	Q96PF6	Q96PF6 homo sapien
29	352	47.7	214	11	Q9RIAS	Q9RIAS mus musculus
30	346.5	47.0	235	11	Q9IWI2	Q9IWI2 mus musculus
31	345.5	46.8	112	11	Q8K1F3	Q8K1F3 mus musculus
32	344.5	46.7	112	11	Q8K1F2	Q8K1F2 mus musculus
33	336	45.5	111	11	Q920E9	Q920E9 mus musculus
34	335.5	45.5	134	11	Q8VDD0	Q8VDD0 mus musculus
35	331	44.9	298	11	Q9QYF0	Q9QYF0 mus musculus
36	330	44.7	108	11	Q8VIJ0	Q8VIJ0 mus musculus
37	329	44.6	111	11	Q8I1U6	Q8I1U6 mus musculus
38	329	44.6	148	11	Q8K122	Q8K122 mus musculus
39	327.5	44.4	106	5	Q9U410	Q9U410 schistosoma
40	325	44.0	127	11	Q925S9	Q925S9 mus musculus
41	322	43.6	97	11	Q9UL76	Q9UL76 mus musculus
42	321.5	43.6	243	11	Q7TQM2	Q7TQM2 mus musculus
43	319	43.2	101	11	Q9UL78	Q9UL78 mus musculus
44	318.5	43.2	112	11	Q8K1F0	Q8K1F0 mus musculus
45	318	43.1	109	11	Q920E6	Q920E6 mus musculus

ALIGNMENTS

RESULT 1					
Q9UL78					
ID	Q9UL78	PRELIMINARY;	PRT;	109 AA.	
AC	Q9UL78;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).				
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
EX	MEDLINE=98277139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035036; AAD56272.1; -.				
DR	PIR; A30601; A30601.				
DR	PIR; A30608; A30608.				
DR	PIR; B30601; B30601.				
DR	PIR; B30607; B30607.				
DR	PIR; B30601; C30601.				
DR	PIR; C30607; C30607.				
DR	PIR; C30608; C30608.				
DR	PIR; C30601; D30601.				
DR	PIR; D30607; D30607.				
DR	PIR; D30608; D30608.				
DR	PIR; F30607; F30607.				
DR	PIR; F30608; F30608.				
DR	PIR; G30601; G30601.				
DR	PIR; G30608; G30608.				
DR	PIR; H30607; H30607.				
DR	PIR; H30608; H30608.				
DR	PIR; I30601; I30601.				

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DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 109 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 69.5%; Score 505.5; DB 4; Length 109;
Best Local Similarity 91.8%; Pred. No. 6.3e-44;
Matches 101; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASSRATGIP 60

QY 81 HRFSGSGGTFTLTISRLEPEDFAVYCCQYGTSAITFGGKTKVEIKR 130
Db 61 DRFSGSGGTFTLTISRLEPEDCAVYCCQYGGSP-LTFGGTKVEIKR 109

RESULT 2
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=9614934;
PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Bernay S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 109 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7D7D9C83 CRC64;

Query Match 65.5%; Score 483.5; DB 4; Length 109;
Best Local Similarity 87.3%; Pred. No. 1.1e-41;
Matches 96; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 21 EIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQKPGQAPRLIYGASSRATDIP 80
Db 1 EIVLTQPGTSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGSSRATGIP 60

QY 81 HRFSGSGGTFTLTISRLEPEDFAVYCCQYGTSAITFGGKTKVEIKR 130
Db 61 DRFSGSGGTFTLTISRLEPEDFAVYCCQYGTSSIFTFGGKTKVDIKR 109

us-10-044-569b-8.rpt

RESULT 3
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=12477932;
PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uesdin T.B., Tothiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gumarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
MEDLINE=9614934;
PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Bernay S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 109 1
FT NON_TER 109 109
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 64.9%; Score 479; DB 4; Length 234;
Best Local Similarity 68.5%; Pred. No. 8.6e-41;
Matches 98; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQK 60
Db 1 MRVPAQLGLLLMLPGARCAIRMTQSPSSFSASTGDRVITCRASQSGS-YLAWYQK 59

QY 61 PCQAPRLIYGASSRATDIPHRFSGSGGTFTLTISRLEPEDFAVYCCQYGTSAITF 120
Db 60 PKAPQLIYAASLTQSGVPSRFSAGSGTDTLISICLOSEDFATYCCQYGTYP-WTF 118

QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
Db 119 GGGTKVEIKRTVAAPSVFIFPPS 141

RESULT 4
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=9614934;
PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Bernay S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 109 1
FT NON_TER 109 109
SQ SEQUENCE 239 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH03814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40357; S40357.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 62.4%; Score 460.5; DB 4; Length 239;
Best Local Similarity 62.6%; Pred. No. 6.8e-39;
Matches 92; Conservative 22; Mismatches 28; Indels 5; Gaps 2;

QY 1 METPAQLLLFLLMLPDTTGTGIVLTQPGTSLSPGERATLSRASQSVASA----YLAW 56
DB 1 MRLPAQLGLLMLVWSGSDIWMVQSPISLPVTPGEPASISCRSSQSLHSDGYNLDM 60
QY 57 YQKPGQAPRLIYGASSRATDIPHRFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 116
DB 61 YLQKPGQSPOLLVYLGNSRASGVDRFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 119
QY 117 LLTFGGGKVEIKRTVAAPSVFIFPPS 143
DB 120 PQTFGGGKVEIKRTVAAPSVFIFPPS 146

RESULT 5
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH03814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40357; S40357.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 61.7%; Score 455; DB 4; Length 236;
Best Local Similarity 65.7%; Pred. No. 2.5e-38;
Matches 94; Conservative 16; Mismatches 31; Indels 2; Gaps 2;

QY 1 METPAQLLLFLLMLPDTTGTGIVLTQPGTSLSPGERATLSRASQSVASA---ASAYLAW 60
DB 3 MRLPAQLGLLMLVWSGSDIWMVQSPISLPVTPGEPASISCRSSQSLHSDGYNLDM 61
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 120
DB 62 PGKAPKSLIYGASSLQSGVQSKFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 120
QY 121 GGGTKVRIKRTVAAPSVFIFPPS 143
DB 121 GGGTKVRIKRTVAAPSVFIFPPS 143

RESULT 6
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S34095; S34095.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 60.1%; Score 443.5; DB 4; Length 239;
Best Local Similarity 59.2%; Pred. No. 3.7e-37;
Matches 87; Conservative 27; Mismatches 28; Indels 5; Gaps 2;

QY 1 METPAQLLLFLLMLPDTTGTGIVLTQPGTSLSPGERATLSRASQSV----ASAYLAW 56
DB 1 MRLPAQLGLLMLVWSGSDIWMVQSPISLPVTPGEPASISCRSSQSLHSDGYNLDM 60
QY 57 YQKPGQAPRLIYGASSRATDIPHRFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 116
DB 61 PQKPGQSPOLLVYLGNSRASGVDRFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 119
QY 117 LLTFGGGKVEIKRTVAAPSVFIFPPS 143
DB 117 LLTFGGGKVEIKRTVAAPSVFIFPPS 143

and mouse cDNA sequences."
proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BF4ED23084BC6 CRC64;

Query Match 61.7%; Score 455; DB 4; Length 236;
Best Local Similarity 65.7%; Pred. No. 2.5e-38;
Matches 94; Conservative 16; Mismatches 31; Indels 2; Gaps 2;

QY 1 METPAQLLLFLLMLPDTTGTGIVLTQPGTSLSPGERATLSRASQSVASA---ASAYLAW 60
DB 3 MRLPAQLGLLMLVWSGSDIWMVQSPISLPVTPGEPASISCRSSQSLHSDGYNLDM 61
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 120
DB 62 PGKAPKSLIYGASSLQSGVQSKFSGSGGTDTLTISRLEPDAFYVYCOOYGTSA 120
QY 121 GGGTKVRIKRTVAAPSVFIFPPS 143
DB 121 GGGTKVRIKRTVAAPSVFIFPPS 143

"Generation and initial analysis of more than 15,000 full-length human
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Db 120 PSTFGGQTKLEIKRTVAAPSVEIFPPS 146
RESULT 7
Q9UL85 ID OSUL85 PRELIMINARY; PRT; 109 AA.
AC OSUL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1843E7C7AFACCC CRC64;

Query Match 59.1%; Score 436.5; DB 4; Length 109;
Best Local Similarity 79.1%; Pred. No. 7e-37;
Matches 87; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

Qy 21 EIVLTQPGTSLSPGERATLSRASQSVASAVLAWYQKPGQAPRLIYGASSRATDIP 80
1 EIVMTQPAFLVSPGERATLSWASQSI--SSNLAWYQKPGQAPRLIYGASTRATGIP 59
Db 81 HRFSGSGGDTFTLTISRLEPEDFVAVYQYQYTSALLTFGGTKVEIKR 130
60 ARFSGSGSGTEFTLTISLSQSEDFALYHCQYNSWPPLTFGGTKVEIKR 109

RESULT 8
Q7SZ36 ID Q7SZ36 PRELIMINARY; PRT; 237 AA.
AC Q7SZ36;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RN SEQUENCE FROM N.A.

RC RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillius D.E., Schnarch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054155; AAH54155.1; -.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26300 MW; 47BD0D2639CB436 CRC64;

Query Match 56.6%; Score 418; DB 13; Length 237;
Best Local Similarity 62.9%; Pred. No. 1.5e-34;
Matches 88; Conservative 16; Mismatches 32; Indels 4; Gaps 2;

Qy 7 LLFILLMLPDTTGEIVLTQPGTSLSPGERATLSRASQSV--SAYLAWYQKPGQ 63
Db 7 LLPILMLWLGSGYGVLTQSPDYVSPGETVTLTKASSVAIGSTIYLHWYQKSGQ 66
Qy 64 APRLLIYGASSRATDIPHRFSGSGGDTFTLTISRLEPEDFVAVYQYQYTSALLTFGGG 123
Db 67 VPKLIIYLVNTHRGTHGTPERISGSGSGDTFTLTISRMEADADYVCOQ--SRSDPLTFGKG 125
Qy 124 TKVEIKRTVAAPSVEIFPPS 143
Db 126 TRVELKENDAKPAVFIKPS 145

RESULT 9
Q9NM37 ID Q9NM37 PRELIMINARY; PRT; 238 AA.
AC Q9NM37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020355; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
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DR	PIR; E28833; E28833.	
DR	PIR; F32530; F32530.	
DR	PIR; H31485; H31485.	
DR	PIR; PH0106; PH0106.	
DR	PIR; PH1030; PH1030.	
DR	PIR; PH1031; PH1031.	
DR	PIR; PH1034; PH1034.	
DR	PIR; PL0257; PL0257.	
DR	PIR; PT0359; PT0359.	
DR	PIR; S07455; S07455.	
DR	PIR; S16112; S16112.	
DR	PIR; S26334; S26334.	
DR	PIR; S33750; S33750.	
DR	PIR; S60066; S60066.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 2.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG LIKE; 2.	
DR	PROSITE; PS00290; IG_MHC; 1.	
KW	Hypothetical protein.	
KW	SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;	
SEQ		
	Query Match	56.0%; Score 413; DB 11; Length 238;
	Best Local Similarity	55.8%; Pred. No. 4.8e-34;
	Matches 82; Conservative	28; Mismatches 31; Indels 6; Gaps 3;
QY	1 METPAQLFLLLLWLPDPTTGEIVLTFFPTLTLSPGERATLSCRASQSV---ASAYLAW 56	
Db	1 MKLFRLL-VLMFIPASSDDVVMVTPTLSLFLVSLDQASISCRSSQSLVHNSNGNTYLHW 59	
QY	57 YQQRPGGAPRLLIYGASSRATDIPHFSGSGSGTFTLTLSLEPEDFAVYVYCOQYGTS 116	
Db	60 YLQRPGGSPKLLIYKSNRSGVDFRPSGSGSGTFTLTLSKISVEADLGVFCSQ-STHV 118	
QY	117 LLTFGGGKVEIKRTVAAPSVFIFFPS 143	
Db	119 PPTFGGKLEIKRADAAPTVSIFPPS 145	
RESULT 11		
Q9UL83	PRELIMINARY; PET; 108 AA.	
ID	Q9UL83	
AC	Q9UL83;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-NAV-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Myosin-reactive immunoglobulin light chain variable region (fragment).	
DE	DE	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
DR	EMBL; AF035031; AA056267.1; -.	
DR	PIR; B30609; B30609.	
DR	PIR; C30609; C30609.	
DR	PIR; D30609; D30609.	
DR	PIR; S34098; S34098.	
DR	PIR; S34099; S34099.	
DR	HSP; P80362; 1WTL.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	

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DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match
Best Local Similarity 55.7%; Score 411; DB 4; Length 108;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

QY 21 EIVLTPPGTSLSPGERATLSRASQSVASAYLAWYQKPGQAPRLIYGASSRATDIP 80
DB 1 EIVWTSPTLSVSPERATLSRASQSVSSNLAWYQKPGQAPRLIYCASTRATGIP 59

QY 81 HRFSGSGGDFLTISRLEPEDFVAVYCCQYGTSAALLTFGGGKVEIKR 130
DB 60 ARFSGSGGTFTLTSSQLQFEDFVAVYCOHYNWP-FTFGPGTKVDIKR 108

RESULT 12
Q7TS98 PRELIMINARY; PRT; 236 AA.
ID Q7TS98
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of l16NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; -.
SQ SEQUENCE 236 AA; 26454 MW; 2C596EBF5EA10F4C CRC64;

Query Match
Best Local Similarity 55.1%; Score 407; DB 11; Length 236;
Matches 80; Conservative 23; Mismatches 38; Indels 2; Gaps 2;

QY 1 METPAQLFLLLWLPDTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQK 60
DB 3 MRTPAQFLGILLWFPQKCDIKMTQSPSSMYASLGERVTITCKASQDI-NSYLSWFOK 61

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGTDFTLISRLEPEDFVAVYCCQYGTSAALLTF 120
DB 62 PGKSPKTLIYRANRLVDGVSPFRSGSGGQDYSLTSSLESDDTATYCYLQHGESP-YTF 120

QY 121 GGGTKVEIKTVAAPSFIIPPS 143
DB 121 GGGTKLEIKRADRAPTVSIIPPS 143

RESULT 13
Q7TMK3 PRELIMINARY; PRT; 236 AA.
ID Q7TMK3
AC Q7TMK3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Breast tumor;
RA Klauner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Parey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC055906; AAK55906.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26299 MW; 0DB03489AAA6396F CRC64;

Query Match
Best Local Similarity 54.7%; Score 404; DB 11; Length 236;
Matches 81; Conservative 21; Mismatches 39; Indels 2; Gaps 2;

QY 1 METPAQLFLLLWLPDTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQK 60
DB 3 MRAPQFGILLWFPQKCDIKMTQSPSSMYASLGERVTITCKASQDIKS-YLSWYQK 61

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGGTDFTLISRLEPEDFVAVYCCQYGTSAALLTF 120
DB 62 PWKSPKTLIYATSLADGVSPFRSGSGGQDYSLTSSLESDDTATYCYLQHGESP-YTF 120

QY 121 GGGTKVEIKTVAAPSFIIPPS 143
DB 121 GSGTKLEIKRADRAPTVSIIPPS 143

RESULT 14
Q8K0F8 PRELIMINARY; PRT; 239 AA.
ID Q8K0F8
AC Q8K0F8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC031498; AAK31498.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
```

Search completed: April 5, 2004, 13:42:06
CDB time : 30.4873 secs

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DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGC1; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00061; ADH_SHORT; 1.  
DR PROSITE: PS00835; IG_LIKE; 2.  
DR PROSITE: PS00290; IG_MHC; 1.  
KW Hypothetical protein_  
SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;  
  
Query Match 52.7%; Score 389; DB 11; Length 234;  
Best Local Similarity 55.9%; Pred. No. 1.3e-31;  
Matches 80; Conservative 21; Mismatches 40; Indels 2; Gaps 2;  
  
QY 1 METPAQLFLLLMLPDTTGEIVLTQPGTGLSPGERATLSCRASQSV-----ASAYLAW 56  
Db 1 MMSPAQLFLLLVLSIQINGDVVMTQPLTSLVIGQPASISCSQSLSFYNGKMYLSW 60  
  
QY 57 YQKPGQAPRLIYGASRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSA 116  
Db 61 LLQRPQSPKRLISLVSKLDSGVPDRFSGSGGTDFLTISRVEAEDLGVYICLQ-STHF 119  
  
QY 117 LLFPGGKVEIKRTVAAPSVFIFPPS 143  
Db 120 PYTFGGTKLEIKRAADAAPTVISIFPPS 146  
  
RESULT 15  
Q8VCP0 PRELIMINARY; PRT; 234 AA.  
AC Q8VCP0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg P.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019474; AAH19474.1; -.  
DR PIR; B47329; B47329.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;  
  
Query Match 52.7%; Score 389; DB 11; Length 234;  
Best Local Similarity 55.9%; Pred. No. 1.3e-31;  
Matches 80; Conservative 21; Mismatches 40; Indels 2; Gaps 2;  
  
QY 1 METPAQLFLLLMLPDTTGEIVLTQPGTGLSPGERATLSCRASQSVASAYLAWYQK 60  
Db 1 MSVFTQVLGLLLCLTGARCDIQLTQSPASLSASVGETVITCRASNIYS-YLAWYQK 59  
  
QY 61 PQQAPRLIYGASRATDIPHRFSGSGGTDFLTISRLEPEDFAVYCCQYGTSA 120  
Db 60 QGKSPQLLVYNAKTLADGVPRFSGSGGTQFSLKINSLOPEDFGSYICQH-SGIPFTF 118  
  
QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143  
Db 119 GSGTKLEIKRAADAAPTVISIFPPS 141
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 5, 2004, 12:09:21 ; Search time 46.2149 Seconds
(without alignments)
874.270 Million cell updates/sec

Title: US-10-044-569B-8
Perfect score: 738
Sequence: 1 METPAQLLELLMLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	738	100.0	143	4 AAB47061	Aab47061 Light cha
2	738	100.0	143	5 AAO18879	Aao18879 Human XRI
3	667	90.4	234	7 ADE28481	Ade28481 Human ant
4	666.5	90.3	235	3 AAY93702	Aay93702 The kappa
5	666.5	90.3	235	3 AAY93729	Aay93729 The kappa
6	666.5	90.3	235	6 AAE35884	Aae35884 Human 4.1
7	660	89.4	236	5 AAU74299	Aau74299 Anti-huma
8	658.5	89.2	235	6 ABP71366	Abp71366 Anti-OPGL
9	654.5	88.7	142	4 AAB47060	Aab47060 Light cha
10	654.5	88.7	142	5 AAO18877	Aao18877 Human B02
11	654.5	88.7	233	3 AAY93704	Aay93704 The kappa
12	654.5	88.7	233	3 AAY93731	Aay93731 The kappa
13	654.5	88.7	233	6 AAE35886	Aae35886 Human 4.8
14	652	88.3	236	5 AAU74301	Aau74301 Anti-huma
15	649.5	88.0	150	2 AAU0069	Aau0069 Human mon
16	649.5	88.0	150	4 AAE00946	Aae00946 Human mon
17	645	87.4	234	3 AAY93733	Aay93733 The kappa
18	645	87.4	234	3 AAY93708	Aay93708 The kappa
19	645	87.4	234	6 AAE35888	Aae35888 Human 6.1
20	641.5	86.9	150	7 ABU10485	Abu10485 Human C-a
21	627	85.0	234	7 ADE28473	Ade28473 Human ant
22	622	84.3	131	6 ABP57366	Abp57366 Anti-TRAI
23	619.5	83.9	130	6 ADA43061	Ada43061 Human ant
24	619.5	83.9	238	6 ABR41582	Ab41582 Human DIT
25	614	83.2	234	3 AAY92239	Aay92239 Human bon

ALIGNMENTS

RESULT 1

AAB47061
ID AAB47061 standard; protein; 143 AA.

XX
AC AAB47061;

DT 08-MAY-2001 (first entry)

DE Light chain variable region VL of KRIX1.

XX Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;

XX complementarity determining region; CDR; WAB; BO2C11;

XX conformational epitope; factor VIII; KRIX1; von Willebrand factor;

XX hemostasis; intravascular coagulation; arterial thrombosis;

XX arterial restenosis; venous thrombosis; arteriosclerosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 43..54

FT Domain /label= CDR1

FT Domain 59..75

FT Domain /label= CDR2

FT Domain 109..118

FT Domain /label= CDR3

WO200104269-A1.

PD 18-JAN-2001.

XX 13-JUL-2000; 2000WO-EP006677.

XX 14-JUL-1999; 99GB-00016450.

PR 14-JUL-1999; 99US-C143891P.

XX (LEUV-) LEUVEN RES & DEV VZW.

XX Jacquemin MG, Saint-Remy JR;

XX WPI; 2001-138333/14.

DR N-PSDB; AAC85454.

XX Novel cell lines for producing monoclonal antibodies that bind to a
factor involved in hemostasis and coagulation cascade, useful for
treating and preventing coagulation disorders.

PS Example 5; Fig 9; 55pp; English.

XX

Aag71272 Human gen.
Abg63490 Human alb
Abj36930 Anti-CD40
Aaw11155 Anti-lung
Aar38672 vk325-Jk2
Adc61062 Human ant
Aao14066 Light cha
Abu08018 Human mon
Aar41286 F105 rear
Add01357 Human imm
Aar38673 F105VK-F1
Aam24101 Human EST
Aau33249 Novel hum
Aau14463 Human nov
Aau14461 Human nov
Aau14464 Human nov
Aab99378 Human int
Aab75011 Anti-IL8
Aab99397 Human int

CC This sequence represents the light chain variable region of the
CC monoclonal antibody (WAb), KR1X1. This WAb produced by the cell line of
CC the invention, specifically recognises the wild type factor VIII light
CC chain. KR1X1 can be used to inhibit the binding of factor VIII to von
CC Willebrand factor in a dose dependant manner. The new cell line KR1X 1,
CC is deposited with the Belgian Coordinated Collections of Micro-organisms,
CC under accession number LMBP 5089CB. KR1X1, or fragments of it, optionally
CC with a thrombolytic agent, are useful for the treatment and/or prevention
CC of hemostasis, coagulation disorder or thrombotic pathologic condition
CC such as intravascular coagulation, arterial thrombosis, arterial
CC restenosis, venous thrombosis or arteriosclerosis, and attenuation of
CC coagulation in a mammal. An effective and safe antithrombotic therapy is
CC provided which reduces the risk of bleeding in mammals, more particularly
CC in humans
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 738; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 3e-47;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
QY 61 PGQAPRLLIYGASRATDIPHRFSGSGGTDFTLTISRLEPDPFVAVYCCQYGTSAALLTF 120
DB 61 PGQAPRLLIYGASRATDIPHRFSGSGGTDFTLTISRLEPDPFVAVYCCQYGTSAALLTF 120
QY 121 GGGTKVEIKRTVAAPSVFIIPPPS 143
DB 121 GGGTKVEIKRTVAAPSVFIIPPPS 143

RESULT 2
AAO18879
ID AAO18879 standard; protein; 143 AA.
XX AAO18879;
XX AAO18879;
DT 07-NOV-2002 (first entry)
XX Human KR1X1 light chain variable region.
XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
XX variable region; factor VIII inhibitor; sepsis; septic shock;
KW thrombus formation; systemic inflammatory response syndrome; CDR;
KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;
KW complementarity determining region; antibacterial; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 43..54
FT /label= CDR1
FT Region 69..75
FT /label= CDR2
FT Region 108..117
FT /label= CDR3
XX
XX EPI222929-A2.
XX
XX 17-JUL-2002.
XX
XX 11-JAN-2002; 2002EP-00447005.
XX
XX 11-JAN-2001; 2001US-0261405P.
XX
XX (COLL-) COLLEN RES FOUND VZW D.
XX
XX Jacquemin MG, Saint-Remy JR;
XX
XX WPI; 2002-610270/66.
DR

DR N-PSDB; AAL49257.
XX Pharmaceutical composition for treating systemic inflammatory response
XX syndrome, sepsis, septic shock and/or thrombus formation in
XX microvasculature in mammals, comprises a partial inhibitor of factor
XX VIII.
XX Disclosure; Fig 13; 4ipp; English.
XX The present invention relates to a pharmaceutical composition for the
XX prevention and/or treatment of systemic inflammatory response syndrome
XX (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
XX and disseminated intravascular coagulation in mammals, comprising as an
XX active ingredient a partial inhibitor of factor VIII, in admixture with a
XX carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
XX present sequence is the light chain variable region of KR1X1
SQ Sequence 143 AA;

Query Match 100.0%; Score 738; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 3e-47;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
QY 61 PGQAPRLLIYGASRATDIPHRFSGSGGTDFTLTISRLEPDPFVAVYCCQYGTSAALLTF 120
DB 61 PGQAPRLLIYGASRATDIPHRFSGSGGTDFTLTISRLEPDPFVAVYCCQYGTSAALLTF 120
QY 121 GGGTKVEIKRTVAAPSVFIIPPPS 143
DB 121 GGGTKVEIKRTVAAPSVFIIPPPS 143

RESULT 3
ADE28481
ID ADE28481 standard; protein; 234 AA.
XX ADE28481;
XX ADE28481;
DT 29-JAN-2004 (first entry)
XX Human anti-CD40 antibody 24-2-1 full length light chain protein.
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; light chain; 24-2-1.
XX
XX Homo sapiens.
XX
XX WO2003040170-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-US036107.
XX
XX 09-NOV-2001; 2001US-0348980P.
XX
XX (PFIZ) PFIZER PROD INC.
XX (ABGE-) ABGENIX INC.
XX
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
XX WPI; 2003-441521/41.
XX
XX N-PSDB; ADE28480.
XX
XX New chimeric or human monoclonal antibody or its antigen-binding portion
XX that specifically binds to and activates human CD40, useful for enhancing
XX an immune response in a human, or treating cancer, HIV, neutropenia or
XX viral infections.
PT

XX Claim 7; SEQ ID NO 88; 177pp; English.

PS The invention relates to a novel chimeric or human monoclonal antibody or

XX its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40

CC antibody full length light chain protein of the invention.

XX Sequence 234 AA;

Query Match 90.4%; Score 667; DB 7; Length 234;

Best Local Similarity 92.3%; Pred. No. 8.3e-42;

Matches 132; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60

DB 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSVSTYLAAYQOK 60

QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120

DB 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQY--SSLFTF 118

QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143

DB 119 GPGTKVDIKRTVAAPSVFIFPPS 141

RESULT 4

AAAY93702

ID AAY93702 standard; protein; 235 AA.

AC AAY93702;

XX 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.1.1.

XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;

KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

XX WO200037504-A2.

PN 29-JUN-2000.

XX 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46865.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.

XX Claim 3; Fig 1A; 157pp; English.

CC The present sequence represents a kappa chain of an antibody of the

CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)

CC -4. Antibodies of the invention are composed of a heavy chain variable

CC region, comprising a modified contiguous sequence from a FR1-FR3 sequence

CC encoded by a human VH3-33 family gene. The modifications are contained in

CC CDR1, CDR2 and/or framework regions. The antibodies may be used to

CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity

CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and

CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be

CC used to up-regulate immune system to up-regulate immunodeficient

CC disorders

XX Sequence 235 AA;

Query Match 90.3%; Score 666.5; DB 3; Length 235;

Best Local Similarity 91.6%; Pred. No. 9.1e-42;

Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60

DB 1 METPAQLLELLLLWLPDITTEGEIVLTQPGTSLSPGERATLSCRASQSSSFLAWYQQR 60

QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120

DB 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSP-WTF 119

QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143

DB 120 GGGTKVEIKRTVAAPSVFIFPPS 142

RESULT 5

AAAY93729

ID AAY93729 standard; protein; 235 AA.

AC AAY93729;

XX 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.1.1.

XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;

KW proliferative disorder; cancer; immunodeficient disorder.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..20

XX /note= "signal peptide"

XX WO200037504-A2.

PN 29-JUN-2000.

XX 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

PI Corvalan JR;

XX WPI; 2000-442647/38.

DR N-PSDB; AAA46893.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

PT -4 containing specified heavy and light chain sequences, useful for

PT treating, e.g. immune disorders.

XX Claim 3; Fig 22g; 157pp; English.

XX The present sequence represents a kappa chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
 CC -4. Antibodies of the invention are composed of a heavy chain variable
 CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
 CC encoded by a human VH3-33 family gene. The modifications are contained in
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
 CC used to up-regulate immune system to up-regulate immunodeficient
 CC disorders
 XX SQ Sequence 235 AA;

Query Match 90.3%; Score 666.5; DB 3; Length 235;
 Best Local Similarity 91.6%; Pred. No. 9.1e-42;
 Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLFLLLLWLPDTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSP-WTF 120
 DB 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSP-WTF 119
 QY 121 GGGTKVEIKRTVAAPSVFIPTPPS 143
 DB 120 GGGTKVEIKRTVAAPSVFIPTPPS 142

RESULT 6
 AAES5884
 ID AAES5884 standard; protein; 235 AA.
 AC AAES5884;
 DT 17-JUN-2003 (first entry)
 DE Human 4.1.1 anti-CTLA-4 antibody kappa chain.
 XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
 KW cancer.
 KW Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Peptide 1..220
 FT Protein /label= Signal_peptide
 FT 21..235
 FT /note= "Mature anti-CTLA-4 antibody kappa chain"
 XX
 PN EP1262193-A1.
 XX
 PD 04-DEC-2002.
 XX
 PF 23-MAY-2002; 2002EP-00253652.
 XX
 PR 23-MAY-2001; 2001US-0293042P.
 XX
 PA (PFIZ) PFIZER PROD INC.
 XX
 PI Hanson DC, Mueller EE;
 XX
 DR WPI; 2003-131215/13.
 DR N-PSDB; AAD54344.
 XX
 PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
 FT preparation of medicament for the treatment of cancer.
 XX
 PS Disclosure; Fig 1G; 76pp; English.
 XX

CC The invention relates to the use of human anti-cytotoxic T lymphocyte
 CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
 CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
 CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
 CC cancer, cancer of the anal region, stomach cancer, breast cancer,
 CC testicular cancer, uterine cancer, and carcinoma of the fallopian tubes.
 CC The present sequence is human anti-CTLA-4 antibody kappa chain
 XX SQ Sequence 235 AA;

Query Match 90.3%; Score 666.5; DB 6; Length 235;
 Best Local Similarity 91.6%; Pred. No. 9.1e-42;
 Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLFLLLLWLPDTTGEIVLTQPPGTLSPGERATLSRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSP-WTF 120
 DB 61 PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYCCQYGTSP-WTF 119
 QY 121 GGGTKVEIKRTVAAPSVFIPTPPS 143
 DB 120 GGGTKVEIKRTVAAPSVFIPTPPS 142

RESULT 7
 AAU74299
 ID AAU74299 standard; protein; 236 AA.
 XX AAU74299;
 AC AAU74299;
 DT 12-MAR-2002 (first entry)
 DE Anti-human AILIM monoclonal antibody clone Jmab-138, light chain.
 XX
 KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;
 KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
 KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
 KW systemic lupus erythematosus; autoimmune disorder; inflammation;
 KW graft versus host reaction; immune rejection; intestinal immunity;
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 XX
 OS Homo sapiens.
 XX
 FN WO200187981-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 15-MAY-2001; 2001WO-JP004035.
 XX
 PR 18-MAY-2000; 2000JP-00147116.
 PR 30-MAR-2001; 2001JP-00099508.
 XX
 PA (NIBS) JAPAN TOBACCO INC.
 XX
 PI Tsuji T, Tezuka K, Hori N;
 XX
 DR WPI; 2002-075313/10.
 DR N-PSDB; AAS99475.
 XX
 PT New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation.
 XX
 PS Claim 30; Page 284-285; 300pp; English.
 XX
 XX The invention relates to a novel human antibody (I), preferably a human

CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AIIIM). (I) is useful for modulating signal
 CC transduction into a cell mediated by AIIIM, for modulating proliferation
 CC of AIIIM-expressing cells, for modulating production of a cytokine from
 CC AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AIIIM-expressing cells and/or immune cytotoxicity or apoptosis of
 CC AIIIM-expressing cells. (II) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with AIIIM-mediated costimulatory
 CC transduction, and for inhibiting the onset and/or advancement of the
 CC diseases. (I) is useful for suppression, prevention and/or treatment of
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
 CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
 CC host reaction, graft versus host disease, immune rejection, disorders
 CC caused by abnormal intestinal immunity, specifically inflammatory
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
 CC nephritis, vasculitis, and pancreatitis. (II) induces no serious
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse
 CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
 CC AIIIM monoclonal antibody amino acid sequences of the invention

XX SQ Sequence 236 AA;

Query Match 89.4%; Score 660; DB 5; Length 236;

Best Local Similarity 88.8%; Pred. No. 2.8e-41; Indels 0; Gaps 0;

Matches 127; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60

Db 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60

Qy 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFVAVYCOQYQTSALLTF 120

Db 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFVAVYCOQYQTSALLTF 120

Qy 121 GGGTKVEIKRTVAAPSVFIFFPPS 143

Db 121 GGGTKVEIKRTVAAPSVFIFFPPS 143

RESULT 8

ABP71366

ID ABP71366 standard; protein; 235 AA.

XX AC ABP71366;

XX DT 28-APR-2003 (first entry)

XX DE Anti-OPGL-1 antibody kappa light chain.

XX KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;

XX KW antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT Region /note= "IgG2 signal peptide"

FT Region 21..128

FT Region /note= "variable region"

FT Region 129..235

FT Region /note= "constant region"

XX PN WO2003002713-A2.

XX PD 09-JAN-2003.

XX PF 25-JUN-2002; 2002WO-US020181.

XX PR 26-JUN-2001; 2001US-0301172P.

XX XX

(ABGE-) ABGENIX INC.

(AMGE-) AMGEN INC.

PI Boyle WJ, Martin FH, Corvalan JR, Davis GC;

DR WP; 2003-210262/20.

DR N-PSDB; ABZ59148.

XX New antibodies that interact with osteoprotegerin ligands, useful for
 PT treating osteopenic disorders, e.g. osteoporosis, bone loss from
 PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and
 PT osteonecrosis.

XX Claim 1; Fig 4; 144pp; English.

PS The invention relates to antibodies that interact with osteoprotegerin
 CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in
 CC a biological sample. The antibody, or the pharmaceutical composition
 CC comprising the antibody, is also useful for treating osteopenic disorder,
 CC an inflammatory condition with attendant bone loss, an autoimmune
 CC condition with attendant bone loss in a patient or rheumatoid arthritis
 CC in a patient. In particular, the antibody or composition is useful for
 CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
 CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
 CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'
 CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
 CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
 CC kappa light chain

XX SQ Sequence 235 AA;

Query Match 89.2%; Score 658.5; DB 6; Length 235;

Best Local Similarity 91.6%; Pred. No. 3.6e-41; Indels 1; Gaps 1;

Matches 131; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60

Db 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60

Qy 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFVAVYCOQYQTSALLTF 120

Db 61 PGQAPRLIYGASRRATDIPHRFGSGSGTDFTLTISRLEPEDFVAVYCOQYQTSALLTF 120

Qy 121 GGGTKVEIKRTVAAPSVFIFFPPS 143

Db 120 GGGTKVEIKRTVAAPSVFIFFPPS 142

RESULT 9

ABP71366

ID AAB47060 standard; protein; 142 AA.

XX AC AAB47060;

XX DT 08-MAY-2001 (first entry)

XX DE Light chain variable region VL of B02C11.

XX KW Monoclonal antibody; variable region; heavy chain; light chain; VH; VL;

XX KW complementarity determining region; CDR; Mab; B02C11;

XX KW conformational epitope; factor VIII; KRXL1; von Willebrand factor;

XX KW hemostasis; intravascular coagulation; arterial thrombosis;

XX KW arterial restenosis; venous thrombosis; arteriosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 43..54

FT Domain /label= CDR1

FT Domain 69..75

FT Domain /label= CDR2

FT Domain 109..117

FT Domain /label= CDR3

XX WO200104269-A1.
 XX 18-JAN-2001.
 XX 13-JUL-2000; 2000WO-EF006677.
 XX 14-JUL-1999; 99GB-00016450.
 XX 14-JUL-1999; 99US-0143891P.
 XX (LEUV-) LEUVEN RES & DEV VZW.
 XX Jacquemin MG, Saint-Remy JR;
 XX WPI; 2001-138333/14.
 XX N-PSDB; AAC85453.
 XX Novel cell lines for producing monoclonal antibodies that bind to a
 PT factor involved in hemostasis and coagulation cascade, useful for
 FT treating and preventing coagulation disorders.
 XX
 PS Example 5; Fig 7; 55pp; English.
 CC This sequence represents the light chain variable region of the human
 CC monoclonal antibody (Mab), B02C11. B02C11 is a human Mab which recognises
 CC a conformational epitope within the carboxy-terminal of the factor VIII
 CC light chain. B02C11 recognises both the wild type and Arg215His factor
 CC VIII light chains. The Mab produced by the cell line of the invention,
 CC KR1X1, specifically recognises the wild type factor VIII light chain.
 CC KR1X1 can be used to inhibit the binding of factor VIII to von Willebrand
 CC factor in a dose dependant manner. The new cell line KR1X 1, is deposited
 CC with the Belgian Coordinated Collections of Micro-organisms, under
 CC accession number LMBP 5089CB. KR1X1, or fragments of it, optionally with
 CC a thrombolytic agent, are useful for the treatment and/or prevention of
 CC hemostasis, coagulation disorder or thrombotic pathologic condition such
 CC as intravascular coagulation, arterial thrombosis, arterial restenosis,
 CC venous thrombosis or arteriosclerosis, and attenuation of coagulation in
 CC a mammal. An effective and safe antithrombotic therapy is provided which
 CC reduces the risk of bleeding in mammals, more particularly in humans
 CC
 XX SQ Sequence 142 AA;
 Query Match 88.7%; Score 654.5; DB 4; Length 142;
 Best Local Similarity 89.5%; Pred. No. 4.4e-41;
 Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLMLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLFLLLLMLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITTF 120
 DB 61 PGQAPRLIIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSA-ITF 119
 QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
 DB 120 GQGTREIKGTVAAPSVFIFPPS 142
 RESULT 10
 AA018877
 ID AA018877 standard; protein; 142 AA.
 XX AA018877;
 AC AA018877;
 XX 07-NOV-2002 (first entry)
 DT Human B02C11 light chain variable region.
 XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;

KW complementarity determining region; antibacterial; antiinflammatory.
 XX Homo sapiens.
 XX Location/Qualifiers
 FT 43..54
 FT /label= CDR1
 FT 69..75
 FT /label= CDR2
 FT 108..116
 FT /label= CDR3
 XX EPI222929-A2.
 XX 17-JUL-2002.
 XX 11-JAN-2002; 2002EP-00447005.
 XX 11-JAN-2001; 2001US-0261405P.
 XX (COLL-) COLLEN RES FOUND VZW D.
 XX Jacquemin MG, Saint-Remy JR;
 XX WPI; 2002-610270/66.
 XX N-PSDB; AAL49255.
 XX Pharmaceutical composition for treating systemic inflammatory response
 PT syndrome, sepsis, septic shock and/or thrombus formation in
 FT microvasculature in mammals, comprises a partial inhibitor of factor
 PT VIII.
 XX Disclosure; Fig 11; 41pp; English.
 XX The present invention relates to a pharmaceutical composition for the
 CC prevention and/or treatment of systemic inflammatory response syndrome
 CC (SIRS), sepsis, septic shock, thrombus formation in the microvasculature
 CC and disseminated intravascular coagulation in mammals, comprising as an
 CC active ingredient a partial inhibitor of factor VIII, in admixture with a
 CC carrier. Such inhibitors may include the antibodies B02C11 and KR1X1. The
 CC present sequence is the light chain variable region of B02C11
 XX SQ Sequence 142 AA;
 Query Match 88.7%; Score 654.5; DB 5; Length 142;
 Best Local Similarity 89.5%; Pred. No. 4.4e-41;
 Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
 QY 1 METPAQLLFLLLLMLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 DB 1 METPAQLLFLLLLMLPDTTGEIVLTQPGTILSPGERATLSCRASQSVASAYLAWYQOK 60
 QY 61 PGQAPRLIIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSAITTF 120
 DB 61 PGQAPRLIIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGTSA-ITF 119
 QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
 DB 120 GQGTREIKGTVAAPSVFIFPPS 142
 RESULT 11
 AA0193704
 ID AA0193704 standard; protein; 233 AA.
 XX AA0193704;
 AC AA0193704;
 XX 03-OCT-2000 (first entry)
 DT The kappa chain of immunoglobulin clone 4.8.1.
 XX Human; antibody; B02C11; KR1X1; light chain; heavy chain; inflammation;
 KW variable region; factor VIII inhibitor; sepsis; septic shock;
 KW thrombus formation; systemic inflammatory response syndrome; CDR;
 KW disseminated intravascular coagulation; haemophilia A; immunosuppressive;

KW proliferative disorder; cancer; immunodeficient disorder.
XX Homo sapiens.
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647P.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46867.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX Claim 3; Fig 1B; 157pp; English.
XX The present sequence represents a kappa chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-PR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders
XX SQ Sequence 233 AA;
Query Match 88.7%; Score 654.5; DB 3; Length 233;
Best Local Similarity 91.6%; Pred. No. 7e-41;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;
QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPGTLLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQPGTLLSPGERATLSCRT--SVSSSYLAWYQOK 59
QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGSALLTF 120
Db 59 PGQAPRLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGISP-FTF 117
QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
Db 118 GGGTKVEIKRTVAAPSVFIFPPS 140
RESULT 12
AA93731
ID AA93731 standard; protein; 233 AA.
XX AC AA93731;
XX 03-OCT-2000 (first entry)
XX The kappa chain of immunoglobulin clone 4.8.1.
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX proliferative disorder; cancer; immunodeficient disorder.
XX Homo sapiens.
OS

XX Key Location/Qualifiers
FH Peptide 1-20
FT /note= "signal peptide"
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647P.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX Corvalan JR;
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46895.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX Claim 3; Fig 22k; 157pp; English.
XX The present sequence represents a kappa chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-PR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders
XX SQ Sequence 233 AA;
Query Match 88.7%; Score 654.5; DB 3; Length 233;
Best Local Similarity 91.6%; Pred. No. 7e-41;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;
QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPGTLLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQPGTLLSPGERATLSCRT--SVSSSYLAWYQOK 58
QY 61 PGQAPRLIYGASSRATDIPHRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGSALLTF 120
Db 59 PGQAPRLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGISP-FTF 117
QY 121 GGGTKVEIKRTVAAPSVFIFPPS 143
Db 118 GGGTKVEIKRTVAAPSVFIFPPS 140
RESULT 13
AAE35886
ID AAE35886 standard; protein; 233 AA.
XX AC AAE35886;
XX 17-JUN-2003 (first entry)
XX Human 4.8.1 anti-CTLA-4 antibody kappa chain.
XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
XX cancer.
XX Homo sapiens.
OS

XX Key Location/Qualifiers
PH Peptide 1-20
FT /label= Signal_peptide
FT Protein 21..233
XX /note= "Mature anti-CTLA-4 antibody kappa chain"
XX
XX
XX EPI262193-A1.
XX
XX
XX 04-DEC-2002.
XX 23-MAY-2002; 2002EP-00253652.
XX
XX 23-MAY-2001; 2001US-0293042P.
XX (PRIZ) PFIZER PROD INC.
XX
XX Hanson DC, Mueller EE;
XX
XX WPI; 2003-131215/13.
XX
XX DR N-PSDB; AAD54346.
XX
XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
XX preparation of medicament for the treatment of cancer.
XX
XX Disclosure; Fig 1K; 76pp; English.
XX
XX The invention relates to the use of human anti-cytotoxic T lymphocyte
XX antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
XX the treatment of cancer such as bone cancer, pancreatic cancer, skin
XX cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
XX cancer, cancer of the anal region, stomach cancer, breast cancer,
XX testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
XX The present sequence is human anti-CTLA-4 antibody kappa chain
XX
SQ Sequence 233 AA;

Query Match 88.7%; Score 654.5; DB 6; Length 233;
Best Local Similarity 91.6%; Pred. No. 7e-41;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSCRT--SVSSSLAWYQOK 58

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGTDTFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 59 PGQAPRLIYGASSRATGIPDRFSGSGTDTFTLTISRLEPEDFAVYCCQYGTSAALLTF 117

QY 121 GGGTKVEIKRTVAAPSVFIFFPPS 143
DB 118 GGGTKVEIKRTVAAPSVFIFFPPS 140

RESULT 14
AAU74301
ID AAU74301 standard; protein; 236 AA.
XX
XX AAU74301;
XX
XX
XX 12-MAR-2002 (first entry)
XX
XX Anti-human AILIM monoclonal antibody clone Jmab-139, light chain.
XX
XX Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
XX antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;
XX immunosuppressive; dermatological; antiinflammatory; hepatotropic;
XX activation inducible lymphocyte immunomodulatory molecule; AILIM;
XX monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
XX multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
XX allergic contact-type dermatitis; chronic inflammatory dermatosis;
XX systemic lupus erythematosus; autoimmune disorder; inflammation;
XX graft versus host reaction; immune rejection; intestinal immunity;

KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
XX Homo sapiens.
XX WO200187981-A2.
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-JP004035.
XX
XX 18-MAY-2000; 2000JP-00147116.
XX 30-MAR-2001; 2001JP-00699508.
XX
XX (NISB) JAPAN TOBACCO INC.
XX
XX Tsuji T, Tezuka K, Hori N;
XX
XX WPI; 2002-075313/10.
XX N-PSDB; AAS99477.
XX
XX New human monoclonal antibody that binds to activation inducible
XX lymphocyte immunomodulatory molecule, useful for treating rheumatoid
XX arthritis, multiple sclerosis and inflammation.
XX
XX Claim 30; Page 298-299; 300pp; English.
XX
XX The invention relates to a novel human antibody (I), preferably a human
XX monoclonal antibody which binds to an activation inducible lymphocyte
XX immunomodulatory molecule (AILIM). (I) is useful for modulating signal
XX transduction into a cell mediated by AILIM, for modulating proliferation
XX of AILIM-expressing cells, for modulating production of a cytokine from
XX AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
XX against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
XX AILIM-expressing cells. (I) is useful for treating, preventing or
XX prophylaxis of delayed type allergy. (I) is useful for treating and
XX preventing various diseases associated with AILIM-mediated costimulatory
XX transduction, and for inhibiting the onset and/or advancement of the
XX diseases. (I) is useful for suppression, prevention and/or treatment of
XX rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
XX allergic contact-type dermatitis, chronic inflammatory dermatosis,
XX systemic lupus erythematosus, insulin-dependent diabetes mellitus,
XX psoriasis, autoimmune or allergic disorders, inflammation, graft versus
XX host reaction, graft versus host disease, immune rejection, disorders
XX caused by abnormal intestinal immunity, specifically inflammatory
XX intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
XX nephritis, vasculitis, and pancreatitis. (I) induces no serious
XX immunorejection due to antigenicity to human, i.e., human anti-mouse
XX antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
XX AILIM monoclonal antibody amino acid sequences of the invention
XX
SQ Sequence 236 AA;

Query Match 88.3%; Score 652; DB 5; Length 236;
Best Local Similarity 88.1%; Pred. No. 1.1e-40;
Matches 126; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLMLPDTTGEIVLTQPGTSLSPGERATLSCRASQSVSSSLAWYQOK 60

QY 61 PGQAPRLIYGASSRATDIPHRFSGSGTDTFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 61 PGQAPRLIYGASSRATGIPDRFSGSGTDTFTLTISRLEPEDFAVYCCQYGTSAALLTF 120

QY 121 GGGTKVEIKRTVAAPSVFIFFPPS 143
DB 121 GGGTKVEIKRTVAAPSVFIFFPPS 143

RESULT 15
AAU40069
ID AAU40069 standard; protein; 150 AA.
XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2004, 13:42:12 ; Search time 33.6328 Seconds
(without alignments)
1116.513 Million cell updates/sec

Title: US-10-044-569B-8

Perfect score: 738
Sequence: 1 METPAQLLFLLLLWLPDTTG.....TKVEIKRTVAAPSVFIFFPS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	738	100.0	143	14	US-10-044-569B-8	Sequence 8, Appli
2	666.5	90.3	235	14	US-10-153-382-7	Sequence 7, Appli
3	660	89.4	236	9	US-09-859-053-34	Sequence 34, Appli
4	659.5	89.2	235	12	US-10-180-648-4	Sequence 4, Appli
5	654.5	88.7	142	14	US-10-044-569B-4	Sequence 4, Appli
6	654.5	88.7	233	14	US-10-153-382-11	Sequence 11, Appli
7	652	88.0	236	9	US-09-859-053-38	Sequence 38, Appli
8	649.5	88.0	150	10	US-09-782-397-5	Sequence 5, Appli
9	645	87.4	234	14	US-10-153-382-15	Sequence 15, Appli
10	609	82.5	236	11	US-09-833-245-237	Sequence 237, Appli
11	596	80.8	127	15	US-10-309-762-95	Sequence 95, Appli
12	593.5	80.4	128	15	US-10-309-764-89	Sequence 89, Appli
13	593	80.4	127	15	US-10-309-762-91	Sequence 91, Appli
14	592	80.2	127	15	US-10-309-762-93	Sequence 93, Appli
15	585	79.3	234	10	US-09-848-832-4	Sequence 4, Appli

16	585	79.3	234	14	US-10-225-108A-4	Sequence 4, Appli
17	585	79.3	234	15	US-10-461-148-2	Sequence 2, Appli
18	575.5	78.0	384	15	US-10-291-265-804	Sequence 804, App
19	575.5	78.0	384	15	US-10-291-265-805	Sequence 805, App
20	575.5	78.0	384	15	US-10-291-265-806	Sequence 806, App
21	575.5	78.0	384	15	US-10-291-265-807	Sequence 807, App
22	575	77.9	226	10	US-09-453-234-42	Sequence 42, Appli
23	571	77.4	226	10	US-09-453-234-50	Sequence 50, Appli
24	571	77.4	226	10	US-09-453-234-86	Sequence 86, Appli
25	569	77.1	226	10	US-09-453-234-80	Sequence 80, Appli
26	567	76.8	224	10	US-09-453-234-52	Sequence 52, Appli
27	566	76.7	226	10	US-09-453-234-72	Sequence 72, Appli
28	565.5	76.6	215	15	US-10-307-724-122	Sequence 122, App
29	564	76.4	226	10	US-09-453-234-38	Sequence 38, Appli
30	559.5	75.8	307	15	US-10-291-265-332	Sequence 332, App
31	559.5	75.8	312	15	US-10-291-265-334	Sequence 334, App
32	559	75.7	226	10	US-09-453-234-74	Sequence 74, Appli
33	558	75.6	129	15	US-10-309-764-121	Sequence 121, App
34	556	75.3	129	15	US-10-309-764-105	Sequence 105, App
35	554	75.1	224	10	US-09-453-234-76	Sequence 76, Appli
36	553.5	75.0	215	10	US-09-791-153A-49	Sequence 49, Appli
37	553	74.9	129	15	US-10-309-764-141	Sequence 141, App
38	553	74.9	224	10	US-09-453-234-44	Sequence 44, Appli
39	553	74.9	224	10	US-09-453-234-78	Sequence 78, Appli
40	552	74.8	238	14	US-10-216-484-107	Sequence 107, App
41	552	74.8	238	14	US-10-384-933-107	Sequence 107, App
42	549	74.4	129	15	US-10-309-764-97	Sequence 97, Appli
43	549	74.4	224	10	US-09-453-234-40	Sequence 40, Appli
44	545.5	73.9	130	15	US-10-443-466A-25	Sequence 25, Appli
45	543	73.6	129	15	US-10-309-764-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-10-044-569B-8
Sequence 8, Application US/10044569B
Publication No. US20030175268A1
GENERAL INFORMATION:
APPLICANT: D. Colleen Research Foundation vzw
APPLICANT: Jaquemini, Marc G
APPLICANT: Saint-Remy, Jean-Marie R
TITLE OF INVENTION: Method and pharmaceutical composition for preventing
TITLE OF INVENTION: Method and/or treating systemic inflammatory response syndrome
FILE REFERENCE: C1968
CURRENT APPLICATION NUMBER: US/10/044,569B
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,405
PRIOR FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in version 3.1
SEQ ID NO 8
LENGTH: 143
TYPE: PST
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (127)..(162)
OTHER INFORMATION: complementary determining region number one
FEATURE:
NAME/KEY: misc feature
LOCATION: (205)..(225)
OTHER INFORMATION: complementary determining region number two
FEATURE:
NAME/KEY: misc feature
LOCATION: (325)..(354)
OTHER INFORMATION: complementary determining region number three
US-10-044-569B-8

Query Match 100.0%; Score 738; DB 14; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
DB 121 GGGTKVEIKRTVAAPSVFIPIPPS 143

RESULT 2
US-10-153-382-7
; Sequence 7, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-7

Query Match 90.3%; Score 666.5; DB 14; Length 235;
Best Local Similarity 91.6%; Pred. No. 4.6e-50;
Matches 131; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 119
QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
DB 120 GGGTKVEIKRTVAAPSVFIPIPPS 142

RESULT 3
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 89.4%; Score 660; DB 9; Length 236;
Best Local Similarity 88.8%; Pred. No. 1.7e-49;
Matches 127; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
DB 121 GGGTKVEIKRTVAAPSVFIPIPPS 143

RESULT 4
US-10-180-648-4
; Sequence 4, Application US/10180648
; Publication No. US20040033535A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPGL
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-4

Query Match 89.2%; Score 658.5; DB 12; Length 235;
Best Local Similarity 91.6%; Pred. No. 2.2e-49;
Matches 131; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQPPGTLSPGERATLSGRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 120
DB 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSAALLTF 119
QY 121 GGGTKVEIKRTVAAPSVFIPIPPS 143
DB 120 GGGTKVEIKRTVAAPSVFIPIPPS 142

RESULT 5
US-10-044-569B-4
; Sequence 4, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Colleen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968
; CURRENT APPLICATION NUMBER: US/10/044,569B
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;; CURRENT FILING DATE: 2002-01-11
;; PRIOR APPLICATION NUMBER: US 60/261,405
;; PRIOR FILING DATE: 2001-01-11
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 4
;; LENGTH: 142
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (127)..(162)
;; OTHER INFORMATION: complementary determining region number one
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (205)..(225)
;; OTHER INFORMATION: complementary determining region number two
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (325)..(351)
;; OTHER INFORMATION: complementary determining region number three

US-10-044-569b-4

Query Match 88.7%; Score 654.5; DB 14; Length 142;
Best Local Similarity 89.5%; Pred. NO. 2.9e-49;
Matches 128; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
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QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
DB 61 PQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSA-ITF 119

QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 120 GQTRLEIKGTVAAPSVFIIPPS 142

RESULT 6
US-10-153-382-11
;; Sequence 11, Application US/10153382
;; Publication No. US20030086930A1
;; GENERAL INFORMATION:
;; APPLICANT: PFIZER PRODUCTS INC.
;; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;; FILE REFERENCE: PC23019A
;; CURRENT APPLICATION NUMBER: US/10/153,382
;; CURRENT FILING DATE: 2002-05-22
;; PRIOR APPLICATION NUMBER: 60/293042
;; PRIOR FILING DATE: 2001-05-23
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 11
;; LENGTH: 233
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-153-382-11

Query Match 88.7%; Score 654.5; DB 14; Length 233;
Best Local Similarity 91.6%; Pred. NO. 4.9e-49;
Matches 131; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

QY 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSGRATLSCT--SVSSVLAAYQOK 58
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
DB 59 PQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSA-FTF 117
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143

DB 118 GGGTKVEIKRTVAAPSVFIIPPS 140

RESULT 7
US-09-859-053-38
;; Sequence 38, Application US/09859053
;; Patent No. US20020102658A1
;; GENERAL INFORMATION:
;; APPLICANT: Tezuka, Takashi
;; APPLICANT: Tezuka, Katsumari
;; APPLICANT: Hori, No. US20020102658A1uaki
;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;; OTHER INFORMATION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
;; FILE REFERENCE: 06501-079001
;; CURRENT APPLICATION NUMBER: US/09/859,053
;; CURRENT FILING DATE: 2001-05-16
;; PRIOR APPLICATION NUMBER: JP 2001-99508
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: JP 2000-147116
;; PRIOR FILING DATE: 2000-05-18
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 38
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-859-053-38

Query Match 88.3%; Score 652; DB 9; Length 236;
Best Local Similarity 88.1%; Pred. NO. 8.3e-49;
Matches 126; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60
DB 1 METPAQLLLLLLPDPTTGEIVLTQPGTSLSPGERATLSGRASQSVASAYLAWYQOK 60
QY 61 PQAPRLIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
DB 61 PQAPGLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDPAVYCCQYGTSAITTF 120
QY 121 GGGTKVEIKRTVAAPSVFIIPPS 143
DB 121 GQTKLEIKRTVAAPSVFIIPPS 143

RESULT 8
US-09-782-397-5
;; Sequence 5, Application US/09782397
;; Publication No. US20030021779A1
;; GENERAL INFORMATION:
;; APPLICANT: Dan, Michael D.
;; Maiti, Pradip K.
;; Kaplan, Howard A.
;; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
;; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;; DETECTION OF CANCERS
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Morrison & Foerster LLP
;; STREET: 755 Page Mill Road
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/782,397
;; FILING DATE: 13-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/862,124
;; FILING DATE: 1997-05-22
;; ATTORNEY/AGENT INFORMATION:
;; NAME, Lehabardt, Susan K.
;; REGISTRATION NUMBER: 33,943
;; REFERENCE/DOCKET NUMBER: 31608-20001.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 813-5600
;; TELEFAX: (650) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 150 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-782-397-5

Query Match 88.0%; Score 649.5; DB 10; Length 150;
Best Local Similarity 87.7%; Pred. No. 8.4e-49;
Matches 128; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 1 METPAQLFLLLLPDPTTGIVLTQPGTILSPGERATILSCRASQSVASAYLAWYQOK 60
DB 5 MEFOAQLFLLLLPDPTTGIVLTQPGTILSPGERATILSCRASQSVSSYLAAYQOK 64

QY 61 PQAPRLIYGASRATDIPHRFSGSGTDTFTLTISRLEPEDFVAVYCCQYGTSS---AL 117
DB 65 PQAPRLIYGASTRATDIPHRFSGSGTDTFTLTISRLEPEDFVAVYCCQYGTSPQTPQ 124

QY 118 LTFGGTKVEIKRTVAAPSVFIFFPS 143
DB 125 ITFGGTKVEIKRTVAAPSVFIFFPS 150

RESULT 9
US-10-153-382-15
;; Sequence 15, Application US/10153382
;; Publication No. US20030086930A1
;; GENERAL INFORMATION:
;; APPLICANT: PFIZER PRODUCTS INC.
;; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;; FILE REFERENCE: PC23019A
;; CURRENT APPLICATION NUMBER: US/10/153,382
;; PRIOR FILING DATE: 2002-05-22
;; PRIOR APPLICATION NUMBER: 60/293042
;; PRIOR FILING DATE: 2001-05-23
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 15
;; LENGTH: 234
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-153-382-15

Query Match 87.4%; Score 645; DB 14; Length 234;
Best Local Similarity 90.9%; Pred. No. 3.3e-48;
Matches 130; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

QY 1 METPAQLFLLLLPDPTTGIVLTQPGTILSPGERATILSCRASQSVASAYLAWYQOK 60
DB 1 METPAQLFLLLLPDPTTGIVLTQPGTILSPGERATILSCRASQSVSSYLAAYQOK 59

QY 61 PQAPRLIYGASRATDIPHRFSGSGTDTFTLTISRLEPEDFVAVYCCQYGTSSALLTF 120
DB 60 PQAPRLIYGSSRATGIPDRFSGSGTDTFTLTISRLEPEDFVAVYCCQYGTSP-FTF 118

QY 121 GGGTKVEIKRTVAAPSVFIFFPS 143

DB 119 GPGTKVDIKRTVAAPSVFIFFPS 141

RESULT 10
US-09-833-245-237
;; Sequence 237, Application US/09833245
;; Publication No. US20040010134A1
;; GENERAL INFORMATION:
;; APPLICANT: Human Genome Sciences, Inc.
;; TITLE OF INVENTION: Albumin Fusion Proteins
;; FILE REFERENCE: PF546PCT
;; CURRENT APPLICATION NUMBER: US/09/833,245
;; PRIOR FILING DATE: 2001-04-12
;; PRIOR APPLICATION NUMBER: 60/229, 358
;; PRIOR FILING DATE: 2000-04-12
;; PRIOR APPLICATION NUMBER: 60/256, 931
;; PRIOR FILING DATE: 2000-12-21
;; PRIOR APPLICATION NUMBER: 60/199, 384
;; PRIOR FILING DATE: 2000-04-25
;; NUMBER OF SEQ ID NOS: 2267
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 237
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (3)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (29)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (70)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (73)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (80)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (97)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (112)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (117)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (122)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-237

Query Match 82.5%; Score 609; DB 11; Length 236;
Best Local Similarity 86.8%; Pred. No. 4.4e-45;
Matches 125; Conservative 1; Mismatches 16; Indels 2; Gaps 2;

QY 1 METPAQLFLLLLPDPTTGIVLTQPGTILSPGERATILSCRASQSVASAYLAWYQOK 60
DB 1 MEXPAQLFLLLLPDPTTGIVLTQSPXTILSPGERATILSCRASQSVSSYLAAYQOK 59

QY 61 PQAPRLIYGASRATDIPHRFSGSGTDTFTLTISRLEPEDFVAVYCCQYGTSSALLT 119
DB 60 PQAPRLIYGASRATGIPDRFSGSGTDTFTLTISRLEPEDFVAVYCCQXNPPXYT 119

QY 120 FGGTKVEIKRTVAAPSVFIFFPS 143
DB 120 FGXGKVEIKRTVAAPSVFIFFPS 143

```
RESULT 11
US-10-309-762-95
; Sequence 95, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-95

Query Match      80.4%; Score 596; DB 15; Length 127;
Best Local Similarity 91.5%; Pred. No. 3.1e-44;
Matches 118; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 MEAPAQLLFLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 120
Db 61 PQQAPRLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 118

QY 121 GGGTKVEIK 129
Db 119 GGGTKVEIK 127

RESULT 12
US-10-309-764-89
; Sequence 89, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: AGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-764-89

Query Match      80.4%; Score 593.5; DB 15; Length 128;
Best Local Similarity 91.5%; Pred. No. 5.1e-44;
Matches 118; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSISSALAWYQOK 60

RESULT 13
US-10-309-762-91
; Sequence 91, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-91

Query Match      80.4%; Score 593; DB 15; Length 127;
Best Local Similarity 91.5%; Pred. No. 5.6e-44;
Matches 118; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

QY 1 METPAQLLFLLLWLPDPTTGEIVLTQPGTSLSPGERATLSCRASQSVASAYLAWYQOK 60
Db 1 MEAPAQLLFLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK 60

QY 61 PQQAPRLIYGASSRATDIPHRFSGSGSGTDFLTISRLEPEDFAVYVCOQYGTSAALLTF 120
Db 61 PQQAPRLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYVCOHYGRS--LTF 118

QY 121 GGGTKVEIK 129
Db 119 GGGTKVEIK 127

RESULT 14
US-10-309-762-93
; Sequence 93, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-93
```

US-10-309-762-93

Query Match 80.2%; Score 592; DB 15; Length 127;
Best Local Similarity 90.7%; Pred. No. 6.8e-44;
Matches 117; Conservative 2; Mismatches 8; Indels 2; Gaps 1;
QY 1 METPAQLLFLLLWLPDITTEIIVLTQFPQTLSLSPGERATLSRASQSVASAYLAWYQOK 60
Db 1 METPAQLLFLLLWLPDITTEIIVLTQSPQTLSLSPGERATLSRSTQVYSTYLAWYQOK 60
QY 61 PQAPRLIIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYCTSAALLTF 120
Db 61 PQAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGRS--LTF 118
QY 121 GGTKEIK 129
Db 119 GGTKEIK 127

RESULT 15

US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848,832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-848-832-4

Query Match 79.3%; Score 585; DB 10; Length 234;
Best Local Similarity 83.9%; Pred. No. 5.3e-43;
Matches 120; Conservative 5; Mismatches 16; Indels 2; Gaps 2;
QY 1 METPAQLLFLLLWLPDITTEIIVLTQFPQTLSLSPGERATLSRASQSVASAYLAWYQOK 60
Db 1 MEAPQLLFLLLWLPDITTEIIVLTQSPATLSLSPGERATLACRASOT-ASRYLAWYQOK 59
QY 61 PQAPRLIIYGASSRATDIPHRFSGSGGTDFTLTISRLEPEDFAVYCCQYCTSAALLTF 120
Db 60 PQAPRLIIYDTSNRATGIPARFSGSGGTDFTLTISRLEPEDFAVYCCQ-RFNWPWF 118
QY 121 GGTKEIKRTVAAPSVFIFPPS 143
Db 119 GGTKEIKRTVAAPSVFIFPPS 141

Search completed: April 5, 2004, 13:59:14
Job time : 33.6328 secs